

SEQUENCE LISTING

<110> Genentech, Inc.
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<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

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Ala Lys Lys Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
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Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
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Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
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Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
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Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
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Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
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His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
195 200 205

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<213> Homo sapiens

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Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu			
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Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr			
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Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys			
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<213> Homo sapiens

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Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
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<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 19

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24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 21

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44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

<400> 23

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						20			25					30	

Thr	Asp	Gln	Leu	Ser	Arg	Arg	Gln	Ile	Arg	Glu	Tyr	Gln	Leu	Tyr	Ser
					35			40				45			

Arg	Thr	Ser	Gly	Lys	His	Gly	Asn	Val	Gln	Val	Thr	Gly	Arg	Arg	Ile	Ser	Ala
					50			55				60					

Thr	Ala	Glu	Asp	Gly	Asn	Lys	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp	
					65		70			75			80			

Thr	Phe	Gly	Ser	Arg	Val	Arg	Ile	Lys	Gly	Ala	Glu	Ser	Glu	Lys	Tyr
					85			90				95			

Ile	Cys	Met	Asn	Lys	Arg	Gly	Lys	Leu	Ile	Gly	Lys	Pro	Ser	Gly	Lys
					100			105				110			

Ser	Lys	Asp	Cys	Val	Phe	Thr	Glu	Ile	Val	Leu	Glu	Asn	Asn	Tyr	Thr
					115			120				125			

Ala	Phe	Gln	Asn	Ala	Arg	His	Glu	Gly	Trp	Phe	Met	Ala	Phe	Thr	Arg
					130		135				140				

Gln	Gly	Arg	Pro	Arg	Gln	Ala	Ser	Arg	Ser	Arg	Gln	Asn	Gln	Arg	Glu
					145		150			155		160			

Ala	His	Phe	Ile	Lys	Arg	Leu	Tyr	Gln	Gly	Gln	Leu	Pro	Phe	Pro	Asn
					165			170				175			

His	Ala	Glu	Lys	Gln	Lys	Gln	Phe	Glu	Phe	Val	Gly	Ser	Ala	Pro	Thr
					180			185				190			

Arg	Arg	Thr	Lys	Arg	Thr	Arg	Arg	Pro	Gln	Pro	Leu	Thr		
					195		200				205			

<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 24

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28

<210> 25

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 25
ccggtagacct gcacgtgctt gcaca 24

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

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<400> 26
gcggatctgc cgccctgctca nctggtcggt catggcgccc t 41

<210> 27
<211> 2479
<212> DNA
<213> Homo sapiens

<400> 27
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tccagtcatc ttgattttgc tggttatttt ttttttctt ttcttttcc caccacattg 240
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<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
20 25 30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
 35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
50 55 60

Val	Thr	Val	Leu	Tyr	Leu	His	Asn	Asn	Gln	Ile	Asn	Asn	Ala	Gly	Phe
65					70					75					80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
 145 150 155 160
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
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 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
 210 215 220
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255
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 260 265 270
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 305 310 315 320
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
 325 330 335
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
 340 345 350
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 355 360 365
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
 370 375 380
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
 385 390 395 400
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

405	410	415
Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val		
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Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met		
435	440	445
Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly		
450	455	460
Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu		
465	470	475
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu		
485	490	495
Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala		
500	505	510
Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser		
515	520	525
His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala		
530	535	540
Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser		
545	550	555
Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys		
565	570	575
Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly		
580	585	590
Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln		
595	600	605
Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu		
610	615	620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His		
625	630	635
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu		
645	650	655
His Cys His Thr		
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<210> 29		
<211> 21		
<212> DNA		

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 29

cggtctacctt gttatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 30

gcaggacaac cagataaaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 32

ttcacgggtt gcttttgcgg agctttgaa gtttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

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<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

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					20			25				30			

Ser	Arg	Gly	Arg	His	Ala	Arg	Thr	His	Pro	Gln	Thr	Ala	Leu	Leu	Glu
					35			40				45			

Ser	Ser	Cys	Glu	Asn	Lys	Arg	Ala	Asp	Leu	Val	Phe	Ile	Ile	Asp	Ser
					50			55			60				

Ser	Arg	Ser	Val	Asn	Thr	His	Asp	Tyr	Ala	Lys	Val	Lys	Glu	Phe	Ile
					65			70			75		80		

Val	Asp	Ile	Leu	Gln	Phe	Leu	Asp	Ile	Gly	Pro	Asp	Val	Thr	Arg	Val
					85			90			95				

Gly	Leu	Leu	Gln	Tyr	Gly	Ser	Thr	Val	Lys	Asn	Glu	Phe	Ser	Leu	Lys
					100			105			110				

Thr	Phe	Lys	Arg	Lys	Ser	Glu	Val	Glu	Arg	Ala	Val	Lys	Arg	Met	Arg
					115			120			125				

His	Leu	Ser	Thr	Gly	Thr	Met	Thr	Gly	Leu	Ala	Ile	Gln	Tyr	Ala	Leu
						130		135			140				

Asn	Ile	Ala	Phe	Ser	Glu	Ala	Glu	Gly	Ala	Arg	Pro	Leu	Arg	Glu	Asn
					145			150			155		160		

Val	Pro	Arg	Val	Ile	Met	Ile	Val	Thr	Asp	Gly	Arg	Pro	Gln	Asp	Ser
						165			170			175			

Val	Ala	Glu	Val	Ala	Ala	Lys	Ala	Arg	Asp	Thr	Gly	Ile	Leu	Ile	Phe
						180			185			190			

Ala	Ile	Gly	Val	Gly	Gln	Val	Asp	Phe	Asn	Thr	Leu	Lys	Ser	Ile	Gly
					195			200			205				

Ser	Glu	Pro	His	Glu	Asp	His	Val	Phe	Leu	Val	Ala	Asn	Phe	Ser	Gln
						210		215			220				

Ile	Glu	Thr	Leu	Thr	Ser	Val	Phe	Gln	Lys	Lys	Leu	Cys	Thr	Ala	His
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

225	230	235	240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile			
245		250	255
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser			
260		265	270
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His			
275		280	285
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln			
290		295	300
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala			
305	310	315	320
Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val			
325		330	335
Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu			
340		345	350
Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn			
355		360	365
Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr			
370	375	380	
Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys			
385	390	395	400
Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu			
405		410	415
Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe			
420		425	430
Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu			
435		440	445
Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser			
450	455	460	
Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys			
465	470	475	480
Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu			
485		490	495
His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu			
500		505	510

Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
 515 520 525
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
 545 550 555 560
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
 580 585 590
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
 610 615 620
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
 625 630 635 640
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu
 645 650 655
 Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
 660 665 670
 Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
 675 680 685
 Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
 690 695 700
 Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
 705 710 715 720
 Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735
 Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
 740 745 750
 Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
 755 760 765
 Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
 770 775 780
 Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
 805 810 815

 Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
 820 825 830

 Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
 835 840 845

 Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
 850 855 860

 Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
 865 870 875 880

 Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
 885 890 895

 Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
 900 905 910

 Arg Tyr Arg
 915

 <210> 35
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 35
 gtgaccctgg ttgtgaatac tcc

 <210> 36
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 36
 acagccatgg tctatacgtt gg

 <210> 37
 <211> 45
 <212> DNA
 <213> Artificial Sequence

23

22

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 37
 gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag 45

<210> 38
 <211> 1813
 <212> DNA
 <213> Homo sapiens

<400> 38
 ggagccgccc tgggtgtcag cggctcggt cccgcgcacg ctccggccgt cgccgcaggct 60
 cggcacctgc aggtccgtgc gtccccggc tggcccccgt gactccgtcc cggccaggaa 120
 gggccatgtat ttccctcccg gggcccccgt tgaccactt gctcggttt ttgttccctgg 180
 ggctgagtgc cctcgccccc ccctcgccgg cccagctgca actgcacttg cccgccaacc 240
 ggttgcaggc ggtggaggga ggggaagtgg tgcttccagc gtggtaaaaaacc ttgcacgggg 300
 aggtgttttc atcccccca tgggaggtgc ccttgcgtat gtggttcttc aaacagaaaag 360
 aaaaggagga tcaggtgttg tcctacatca atggggtcac aacaagaaaa cctggagtt 420
 ccttggtcta ctccatgccc tcccggaacc tgccctgcg gctggagggt ctccaggaga 480
 aagactctgg cccctacagc tgctccgtga atgtgcaaga caaacaaggc aaatcttaggg 540
 gccacagcat caaaaacctta gaactcaatg tactggttcc tccagctcct ccattctgcc 600
 gtctccagggttgtccccat gtggggggcaa acgtgaccct gagctgccag tctccaaggaa 660
 gtaagccgc tgcataatc cagtggatc ggcagttcc atccttccag actttcttg 720
 caccagcatt agatgtcata cgtgggtctt taagcctcactt caacccatcg tcttccatgg 780
 ctggagtcata tgcataatc gcccacaatg aggtgggcac tgcccaatgt aatgtgacgc 840
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 tgggtccctgc ccagactcaa gctggctctc tggatgtatg accccaccac tcattggcta 1320
 aaggatttgg ggtctctctt tcctataagg gtcacccata gcacagaggc ctgagtcata 1380
 ggaaagagtc acactcctga cccttagtac tctgcacccca cctcttttta ctgtggggaaa 1440
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 ataacctgtc aggctggctt gtttaggttt tactggggca gaggataggaaatctttat 1740
 taaaactaac atgaaatatg tttgttttc atttgcataat taaaataaag atacataatg 1800
 tttgtatgaa aaa 1813

<210> 39
 <211> 390
 <212> PRT
 <213> Homo sapiens

<400> 39
 Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

1	5	10	15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln			
20	25	30	
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val			
35	40	45	
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln			
50	55	60	
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys			
65	70	75	80
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro			
85	90	95	
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg			
100	105	110	
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val			
115	120	125	
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr			
130	135	140	
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu			
145	150	155	160
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser			
165	170	175	
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro			
180	185	190	
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser			
195	200	205	
Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys			
210	215	220	
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu			
225	230	235	240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly			
245	250	255	
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His			
260	265	270	
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp			
275	280	285	

<400> 42		
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc		50
<210> 43		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 43		
gtgtgacaca gcgtgggc		18
<210> 44		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 44		
gaccggcagg cttctgcg		18
<210> 45		
<211> 25		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 45		
cagcagcttc agccaccagg agtgg		25
<210> 46		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 46		
ctgagccgtg ggctgcagtc tcgc		24
<210> 47		

<211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 47
 ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

 <210> 48
 <211> 2822
 <212> DNA
 <213> Homo sapiens

 <400> 48
 cgccaccact gcggccaccg ccaatgaaac gcctccgct cctagtgggtt ttttccactt 60
 tgttgaatttgc ttccataact caaaaatttgc ccaagacacc ttgtctccca aatgcaaaaat 120
 gtgaaatacg caatggaaatttgc gaaggcctgctt atttgcacat gggattttca ggaaatggtg 180
 tcacaattttg tgaagatgtat aatgtatgtt gaaatttaac tcagtcctgtt ggcggaaaatg 240
 ctaatttgcac taacacagaa ggaagtttattt atttgtatgtt tgtagtgc ttcagatcca 300
 gcagtaacca agacagggtt atactaatatg attggaaaccgtt ctgtatagaa aatgtgaatg 360
 caaactgcca tttagataat gtctgtatag ctgcaaatat taataaaaact ttaacaaaaaa 420
 tcagatccat aaaagaacctt gtggcttgc tacaagaatg ctatagaaat tctgtgacag 480
 atcttcacc aacagatata attacatata tagaaatattt agctgaatca tcttcattac 540
 tagttacaa gaacaacact atctcagcca aggacaccctt ttcttaactca actcttactg 600
 aatttgtaaa aaccgtgaat aattttgttc aaagggatac atttgttagtt tgggacaatg 660
 tatctgtgaa tcataggaga acacatcttta caaaactcat gcacactgtt gaacaagcta 720
 cttaaggat atcccagagc ttccaaaaga ccacagagtt tgatacaat tcaacggata 780
 tagctctcaa agttttcttt ttgttatttcat ataacatgaa acatatttcat cctcatatga 840
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 gcaatgttgc agttgcattt ttatattata agagtattgg tcctttgtt tcattatctg 960
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 tgtcctctgg tccttcattt ggtttaaaatg attataatat tcttacaagg atcactcaac 1320
 taggaataat tatttcaactg atttgtcttgc ccattatgcattt ttttacctt tgggttgcatttt 1380
 gtgaaaattca aaggcaccagg acaacaatttca acaaaaaatctt ttgttgcatttgc ctattttcttgc 1440
 ctgaacttgc tttagtgcattt gggatcaata caaatactaa taagctcttgc ttttcaatca 1500
 ttggccggact gctacactac ttctttttgc ctgctttgc atggatgtgc attgaaggca 1560
 tacatctcta tctcatttttgc ttgttgcatttgc ttttacctt tgggttgcatttt 1620
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 acagatatta tggcacaacc aagtatgtt ggcttagcacc cggaaaacaac ttttatttggaa 1740
 gttttatagg accagcatgc ctaatcatcc ttgtttaatctt cttggcttttgc ggagtcatca 1800
 tatacaaaatgtt ttttcgttgc actgcagggt tgaaaccaga agttagttgc ttttgcatttt 1860
 taaggtcttgc tgcaagagga ggcctcgctt ttctgttgc ttcggcacc acctggatct 1920
 ttgggttctt ccatgttgc tggcatttgc tggtagttttgc ttacctcttgc acagtcagca 1980
 atgcatttcca ggggatgttc attttttat ttttgcattttgc ttttgcattttgc ttttgcatttt 2040
 aagaatatta cagattgttc aaaaatgtcc cctgttgcattttgc tggatgttta aggtaaacat 2100
 agagaatgttgc ggataatttgc aactgcacaa aaataaaaat ttttgcattttgc ttttgcatttt 2160

tgtataaaaa tgactcatca aattatccaa ttattaacta ctagacaaaa agtattttaa 2220
 atcagtttt ctgttatgc tataggaact gtagataata aggtaaaatt atgtatcata 2280
 tagatatact atgttttct atgtgaaata gttctgtcaa aaatagtatt gcagatattt 2340
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 gttgcctttg aaactagtcc cctaccacct cggtaatgag ctccattaca gaaagtggaa 2520
 cataagagaa tgaaggggca gaatatcaaa cagtggaaag ggaatgataa gatgtatttt 2580
 gaatgaactg tttttctgt agactagctg agaaattgtt gacataaaaat aaagaattga 2640
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 agacttctgt ttgctaaatc tggcttttt tctaattttc taaaaaaaaaaa aaaaaggttt 2760
 acctccacaa attgaa 2820
 aa 2822

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

Met	Lys	Arg	Leu	Pro	Leu	Leu	Val	Val	Phe	Ser	Thr	Leu	Leu	Asn	Cys
1															15

5

10

Ser	Tyr	Thr	Gln	Asn	Cys	Thr	Lys	Thr	Pro	Cys	Leu	Pro	Asn	Ala	Lys
															30

20

25

Cys	Glu	Ile	Arg	Asn	Gly	Ile	Glu	Ala	Cys	Tyr	Cys	Asn	Met	Gly	Phe
															45

35

40

Ser	Gly	Asn	Gly	Val	Thr	Ile	Cys	Glu	Asp	Asp	Asn	Glu	Cys	Gly	Asn
															60

50

55

60

Leu	Thr	Gln	Ser	Cys	Gly	Glu	Asn	Ala	Asn	Cys	Thr	Asn	Thr	Glu	Gly
															80

65

70

75

80

Ser	Tyr	Tyr	Cys	Met	Cys	Val	Pro	Gly	Phe	Arg	Ser	Ser	Ser	Asn	Gln
															95

85

90

95

Asp	Arg	Phe	Ile	Thr	Asn	Asp	Gly	Thr	Val	Cys	Ile	Glu	Asn	Val	Asn
															110

100

105

110

Ala	Asn	Cys	His	Leu	Asp	Asn	Val	Cys	Ile	Ala	Ala	Asn	Ile	Asn	Lys
															125

115

120

125

Thr	Leu	Thr	Lys	Ile	Arg	Ser	Ile	Lys	Glu	Pro	Val	Ala	Leu	Leu	Gln
															140

130

135

140

Glu	Val	Tyr	Arg	Asn	Ser	Val	Thr	Asp	Leu	Ser	Pro	Thr	Asp	Ile	Ile
															160

145

150

155

Thr	Tyr	Ile	Glu	Ile	Leu	Ala	Glu	Ser	Ser	Ser	Leu	Leu	Gly	Tyr	Lys
															175

165

170

175

Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr

180	185	190
Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val		
195	200	205
Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys		
210	215	220
Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe		
225	230	235
Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys		
245	250	255
Val Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met		
260	265	270
Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala		
275	280	285
Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser		
290	295	300
Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln		
305	310	315
Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile		
325	330	335
Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys		
340	345	350
Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser		
355	360	365
Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp		
370	375	380
Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser		
385	390	395
Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly		
405	410	415
Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln		
420	425	430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr		
435	440	445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys		
450	455	460

Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
 465 470 475 480

Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
 660 665 670

Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
 675 680 685

Leu Arg
 690

<210> 50
 <211> 589
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (61)

<223> a, t, c or g

<400> 50

tggaaacata tcctccctca tatgaatatg gatggagact acataaatat atttccaaag 60
 ngaaaagccg gcatatggat tcaaattggca atgttcagt tgcatttttta tattataaga 120
 gtattggtcc ct当地gatcc atcatctgac aacttcttat tgaaacctca aaattatgtat 180
 aattctgaag aggagggaaag agtcatatct tcagtaattt cagtcataat gagctcaaacc 240
 ccacccacat tatatgaact tgaaaaata acatttacat taagtcatacg aaaggcaca 300
 gataggata ggagtctatg tggcattttg gaatactcac ctgataccat gaatggcagc 360
 tggcttcag agggctgtga gctgacatac tcaaattgaga cccacacccat atgccgtgt 420
 aatcacctga cacatttgc aattttgatg tcctctggc cttccatttg tattaaagat 480
 tataatattc ttacaaggat cactcaacta ggaataatta tttcactgat ttgtcttgcc 540
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<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 55

ggatctcctg agtcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 56

cctagtttag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

gctcccagcc aagaacctcg gggccgctgc gcgggtgggg a gagttcccc gaaacccggc 60
cgctaagcga ggcctcctcc tcccgagat ccgaacggcc tgggggggt caccggct 120

gggacaagaa gccgcgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180
 aggcggggtg tgagtgggtg tgtgcggggg gcggaggctt gatcaatcc cgataagaaa 240
 tgctcgggtg tcttggcac ctacccgtgg ggccgtaag ggcgtactat ataaggctgc 300
 cggcccgag ccgcgcgc gtcagagcag gagcgtcg tccaggatct agggccacga 360
 ccatcccaac cggcaactca cagccccgca gcgcatccc gtcgcgc gaccccacgc 420
 acccccacg cggagctgc gcgcagagcc ccagggaggt gccatgcgga gcgggtgtgt 480
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 cctgtacacc tccggcccc acgggctctc cagctgcttc otgcgcaccc gtgcgcacgg 660
 cgtcggtggac tgcgcgcgg gccagagcgc gcacagttt ctggagatca aggaagtcgc 720
 tctcgccgacc gtggccatca agggcgtgca cagcgtcg gacccatcc tggccgcgc 780
 cggcaagatg caggggctgc ttcaactc ggaggaagac tggctttcg aggaggagat 840
 ccgcccagat ggctacaatg tgtaccgatc cgagaagcac gcgcctccgg tctccctgag 900
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<210> 59
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 59
 Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
 1 5 10 15

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
 50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
 65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
 85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
 100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Ile Arg Pro
 115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
 130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
 145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
 165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
 180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
 195 200 205

Val Arg Ser Pro Ser Phe Glu Lys
 210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 60

atccgccccag atggctacaa tgtgtta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 61

gcctcccggt ctccctgagc agtgccaaac agcggcagtg ta

42

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 62
 ccagtccggc gacaagcccc aa 22

<210> 63
 <211> 1295
 <212> DNA
 <213> Homo sapiens

<400> 63
 cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacccct 60
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 gctgctgctg cgctacctgg tggtcgccct gggctatcat aaggcctatg gttttctgc 180
 cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggctattt tagcctgcaa 240
 aaccccaaag aagactgtt cctccagatt agagtggaaag aaactgggtc ggagtgtctc 300
 ctttgtctac tatcaacaga ctcttcagg tgatttaaa atcggatctg agatgataga 360
 tttcaatacc cggatcaaaa atgtgacaag aagtgtatgc gggaaatatac gttgtgaagt 420
 tagtgccccca tctgagcaag gcacaaacccct ggaagaggat acagtcaactc tggaagtatt 480
 agtggctcca gcagttccat catgtgaagt acccttcttct gctctgagtg gaactgtggt 540
 agagctacga tgtcaagaca aagaaggaa tccagctctt gaatacacat gtttaagga 600
 tggcatccgt ttgctagaaa atcccgact tggctcccaa agcaccaaca gctcatacac 660
 aatgaataca aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720
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 ctcctccag aagagtaatt ctcatctaa agccacgaca atgagtggaa atgtgcagt 960
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 ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcaactg 1140
 accccggagg cggaggttgc agtgagctga gatcacgcca ctgcagtcca gcctggtaa 1200
 cagagcaaga ttccatctca aaaaataaaaa taaataata aataaataact gtttttacc 1260
 tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
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Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
 35 40 45

 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60

 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80

 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
 85 90 95

 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
 100 105 110

 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
 115 120 125

 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
 130 135 140

 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160

 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
 165 170 175

 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
 180 185 190

 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
 195 200 205

 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
 210 215 220

 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
 225 230 235 240

 Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
 245 250 255

 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
 260 265 270

 Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
 275 280 285

 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
 290 295 300

 Gly Gly Ser Arg Gly Gln Glu Phe

305	310	
<pre> <210> 65 <211> 22 <212> DNA <213> Artificial Sequence </pre>		
<pre> <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe </pre>		
<pre> <400> 65 atcggttgtga agtttagtgcc cc </pre>		22
<pre> <210> 66 <211> 23 <212> DNA <213> Artificial Sequence </pre>		
<pre> <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe </pre>		
<pre> <400> 66 acctgcgata tccaacagaa ttg </pre>		23
<pre> <210> 67 <211> 48 <212> DNA <213> Artificial Sequence </pre>		
<pre> <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe </pre>		
<pre> <400> 67 ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc </pre>		48
<pre> <210> 68 <211> 2639 <212> DNA <213> Homo sapiens </pre>		
<pre> <400> 68 gacatcgaggatggggcttagc actgaaaactg cttttcaaga cgaggaagag gaggagaaaag 60 agaaaagaaga ggaagatgtt gggcaacatt tatttaacat gtcacacagg ccggaccctg 120 gcatcatgct gctattccctg caaatactga agaagcatgg gatttaaata ttttacttct 180 aaataaatga attactcaat ctccatgac catctataca tactccacct tcaaaaagta 240 catcaatatt atatcattaa ggaaatagta accttctctt ctccatatg catgacattt 300 ttggacaatg caattgtggc actggcactt atttcaagtga agaaaaaactt tgtggttcta 360 tggcattcat catttgcacaa atgcaaggcat ctcccttatac aatcagctcc tattgaactt 420 actagcactg actgtgaat ctttaagggc ccattacatt tctgaagaag aaagctaaga 480 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagta 540 </pre>		

aagctgtaga taaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggcccttgg 600
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 aaaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcccttctg 840
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 agggaaatcag catacacaatg aaccccatca ggtgtgactg tgcattccgt tggatgaaca 1620
 tgaacaaaac caacattcga ttcatggagc cagattcact gtttgcgtg gaccacccctg 1680
 aattccaaagg tcagaatgtt cggcaagtgc attcaggga catgatggaa atttgtctcc 1740
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 tagttggcgc tgacttgaag ttgttattga tcaaagtgg a tggatcttt ccacaagata 2040
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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

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1				5										10	15

Thr	Thr	Leu	Val	Gln	Ala	Val	Asp	Lys	Lys	Val	Asp	Cys	Pro	Arg	Leu
				20				25					30		

Cys	Thr	Cys	Glu	Ile	Arg	Pro	Trp	Phe	Thr	Pro	Arg	Ser	Ile	Tyr	Met
				35				40				45			

Glu	Ala	Ser	Thr	Val	Asp	Cys	Asn	Asp	Leu	Gly	Leu	Leu	Thr	Phe	Pro
				50				55				60			

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn
 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
 85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
 115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
 130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
 225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
 260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
 275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
 290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
 305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
 325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

340	345	350
Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn		
355	360	365
Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr		
370	375	380
Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro		
385	390	395
Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met		
405	410	415
Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu		
420	425	430
Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala		
435	440	445
Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu		
450	455	460
Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr		
465	470	475
480		
Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys		
485	490	495
Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys		
500	505	510
Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys		
515	520	525
Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser		
530	535	540
Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr		
545	550	555
560		
Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys		
565	570	575
Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys		
580	585	590
Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn		
595	600	605
Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn		
610	615	620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
 625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
 645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
 660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
 675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
 690 695 700

Thr Asn Met Ser
 705

<210> 70
<211> 1305
<212> DNA
<213> Homo sapiens

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ttaccacgtc tggtggagta gatgaggaat gggctcgta ttatgctgac attccagcat 180
gaatctggta gacctgtggta taaccctgttc cctctccatg tgcctccccc tacaaagttt 240
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ttccctctggg ggtttaaatg tcacctgttag caatgaaat ctcaaggaaa taccttagaga 360
tcttcctccct gaaacagtct tactgtatct ggactccaaat cagatcacat ctattcccaa 420
tgaaattttt aaggacctcc atcaactgag agttctcaac ctgtccaaaa atggcattga 480
gttatcgat gagcatgcct tcaaaggagt agctgaaacc ttgcagactc tggacttg 540
cgacaatcggtt attcaaagtgc tgcacaaaaaa tgcctcaat aacctgaaagg ccaggggccag 600
aattgccaac aaccctggc actgcgactg tactctacag caagttctga ggagcatggc 660
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cctgccaaggc aggccaaaga aacgcaggatga acctgatgtt attagcactg tggatagtg 960
tccaaactga ctgtcattga gaaagaaaaga aagtatgtt cgattgcagt agaaataagt 1020
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cacccttaa ttgtacccccc gatggtatat ttctgagtaa gctactatct gaacattttt 1200
tagatccatc tcactatTTT ataatgaaat ttatTTTTT aattaaaag caaataaaag 1260
cttaactttg aaccatggaa aaaaaaaaaaaa aaaaaaaaaaaa aaaca 1305

<210> 71
<211> 259
<212> PRT
<213> Homo sapiens

<400> 71

Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu			
1	5	10	15
Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser			
20	25	30	
Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val			
35	40	45	
Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro			
50	55	60	
Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro			
65	70	75	80
Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser			
85	90	95	
Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala			
100	105	110	
Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val			
115	120	125	
His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn			
130	135	140	
Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met			
145	150	155	160
Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val			
165	170	175	
Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala			
180	185	190	
Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val			
195	200	205	
Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr			
210	215	220	
Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys			
225	230	235	240
Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser			
245	250	255	
Thr Val Val			

<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

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 cccaggaccg cgctgtctg tgccaccgca agtgccttgt ggcagtcccc gagggcatcc 240
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<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

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Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
 35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
 50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
 100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
 115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
 130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
 145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
 165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
 180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
 210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
 225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
 245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
 260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
 275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
 305 310 315 320

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
 325 330 335

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
 340 345 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
 355 360 365

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
 370 375 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
 385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
 405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
 420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
 435 440 445

Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
 450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
 465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
 485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
 500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
 530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
 545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
 565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

	580	585	590
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<212> DNA			
<213> Artificial Sequence			
<220>			
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oligonucleotide probe			
<400> 74			
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<210> 75			
<211> 23			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Description of Artificial Sequence: Synthetic			
oligonucleotide probe			
<400> 75			
ataccagcta taaccaggct gcg			23
<210> 76			
<211> 52			
<212> DNA			
<213> Artificial Sequence			
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<223> Description of Artificial Sequence: Synthetic			
oligonucleotide probe			
<400> 76			
caacagtaag tggtttgatg ctcttccaaa tcttagagatt ctgatgatttg			50
gg			52
<210> 77			
<211> 22			
<212> DNA			
<213> Artificial Sequence			
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<223> Description of Artificial Sequence: Synthetic			
oligonucleotide probe			

<400> 77	
ccatgtgtct cctcctacaa ag	22
<210> 78	
<211> 23	
<212> DNA	
<213> Artificial Sequence	
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<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 78	
ggaaatagat gtgatctgat tgg	23
<210> 79	
<211> 50	
<212> DNA	
<213> Artificial Sequence	
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<223> Description of Artificial Sequence: Synthetic	
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<400> 79	
cacctgttagc aatgcaaatc tcaaggaaat acctagagat cttcctcctg	50
<210> 80	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
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<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 80	
agcaaccgcc tgaagctcat cc	22
<210> 81	
<211> 24	
<212> DNA	
<213> Artificial Sequence	
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<223> Description of Artificial Sequence: Synthetic	
oligonucleotide probe	
<400> 81	
aaggcgccgt gaaagatgta gacg	24
<210> 82	

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<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 82
gactacatgt ttcaggacct gtacaacctc aagtcaactgg aggttggcga      50

<210> 83
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 83
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aaaca      1685

<210> 84
<211> 398
<212> PRT
<213> Homo sapiens

<400> 84

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Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
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Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
 35 40 45

Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
 50 55 60

Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
 65 70 75 80

Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
 85 90 95

Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
 100 105 110

Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
 115 120 125

Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
 130 135 140

Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
 145 150 155 160

Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
 165 170 175

Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
 180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
 195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
 210 215 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
 225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
 245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
 260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
290 295 300

Met	Gly	Ser	Tyr	Lys	Ala	Tyr	Tyr	Thr	Leu	Asn	Val	Asn	Asp	Pro	Ser
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Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
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<210> 85
<211> 22
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 85
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22

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<210> 86
<211> 22
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 86
aaccttqqaat qtcaccqaaqc tq

22

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<210> 87
<211> 26
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

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<400> 87
cctagcacag tgacgaggga cttggc 26

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 88
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<210> 89
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 89
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90
<211> 2755
<212> DNA
<213> Homo sapiens

<400> 90
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<210> 91
 <211> 696
 <212> PRT
 <213> Homo sapiens

<400> 91
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Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
 35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
 50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
 65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
 85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
 100 105 110
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
 115 120 125
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
 180 185 190
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
 210 215 220
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270
 Ala Pro Pro Ala Gln Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
 290 295 300
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg
 305 310 315 320
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala
 325 330 335
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly
 340 345 350
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
 355 360 365
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
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 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn
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 485 490 495
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala
 500 505 510
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly
 515 520 525
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala
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 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr
 545 550 555 560
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu
 565 570 575
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His
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 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser
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 610 615 620
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<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
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 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
 65 70 75 80
 Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
 85 90 95
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
 100 105 110
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
 115 120 125
 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
 130 135 140
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
 145 150 155 160
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
 165 170 175
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
 180 185 190
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
 195 200 205
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
 210 215 220
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
 225 230 235 240
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
 245 250 255
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
 260 265 270
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
 275 280 285
 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
 290 295 300
 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
 305 310 315 320
 Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
 325 330 335
 Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

340	345	350
Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala		
355	360	365
Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr		
370	375	380
Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe		
385	390	395
Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr		
405	410	415
Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln		
420	425	430
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu		
435	440	445
Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val		
450	455	460
Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu		
465	470	475
Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala		
485	490	
<210> 97		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 97		
tggaaggaga tgcgtatgccca cctg		
<210> 98		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe		
<400> 98		
tgaccagtgg ggaaggacag		

<210> 99		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 99		
acagagcaga ggggccttg		20
<210> 100		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 100		
tcagggacaa gtgggtctc tccc		24
<210> 101		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 101		
tcagggagg agtgtgcagt tctg		24
<210> 102		
<211> 50		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 102		
acagctcccg atctcagtta cttgcattgc ggacgaaatc ggcgctcgct		50
<210> 103		
<211> 2026		
<212> DNA		
<213> Homo sapiens		

<400> 103
cgacgcgtg ggattcagca gtggcctgtg gtcgcagag cagtcctca gggaaacta 60
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tatccccgg ctacctggc cgccccggg cggtcgcgc gtgagaggga ggcgcgggc 180
agccgagcgc cggtgtgagc cagcgtgtgc gccagtgtga gcggcggtgt gacgtgt 240
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ggagagctg gatttattgg cagttaagggt ttccttgag tgtaccctcc aaatagcaaa 480
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gacctcgaga gtgacaacct gtgcgcctat gactttgtgg atgtgtacaa tggccatgcc 600
aatggccagc gcattggccg ctctgtggc actttccgcg ctggagccct tttgtccagt 660
ggcaacaaga ttaggtgca gatgatttct gatgccaaca cagctggca tggcttcatg 720
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gtgttatttg ttccaccttc aagcccttgc cttgtgggtgt tacaatcttgc tcttgcgat 1980
tctaaatcaa tqcttaataaa aatattttta aaggaaaaaaa aaaaaaa 2026

<210> 104

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
1 5 10 15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
20 25 30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
35 40 45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
 50 55 60

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
 65 70 75 80

Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
 85 90 95

His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
 100 105 110

Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
 115 120 125

Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
 130 135 140

Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
 145 150 155 160

Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
 165 170 175

Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
 180 185 190

Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205

Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
 210 215 220

Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
 225 230 235 240

Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
 245 250 255

Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
 260 265 270

Pro Thr Thr Glu Gln Pro Val Thr Thr Phe Pro Val Thr Thr
 275 280 285

Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
 290 295 300

Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly
 305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
 325 330 335

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

340	345	350
-----	-----	-----

Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro
 355 360 365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu
 370 375 380

Asp Gly Arg .Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys
 385 390 395 400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys
 405 410 415

<210> 105
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 105
ccgattcata gacctcgaga gt 22

<210> 106
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 106
gtcaaggagt cctccacaat ac 22

<210> 107
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 107
gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt 45

<210> 108
<211> 1838
<212> DNA

<213> Homo sapiens

<400> 108

cggacgcgtg ggcggacgcg tggcgccccc acggcgcggc cgggctgggg cggtcgcttc 60
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 aagggcctag tcccagctgt gctctgggg ctcagcctct tcctcaacct cccaggac 180
 atctggctcc agccctctcc acctccccag tcttcctccc cgcctcagcc ccatccgtgt 240
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 aactttggag gtggaaacac tgccctggag gaagagaatt tgtccaaata caaagacagt 360
 gagacccgccc tggtagaggt gctggagggt gtgtcagca agtcagactt cgagtgccac 420
 cgccctgtgg agctgagtga ggagctggtg gagagcttgt gtttcacaa gcagcaggag 480
 gccccggacc tcttccactg gctgtgctca gatccctga agctctgtc ccccgccagc 540
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 tacgggggtg aggccctgtgg ccagtgtggc ctggctact ttgaggcaga acgcaacgccc 720
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 tcaaactgtt tgcaatgaa gaagggtctgg gccctgcattt acctcaagtg tgttagacatt 840
 gatgagtgtg gcacagaggg agccaactgt ggagctgacc aattctgtcgt gaacactgag 900
 ggctcctatg agtgcggaga ctgtgccaag gcctgcctag gctgcattggg ggcaggcc 960
 ggtcgctgtg agaagtgttag ccctggctat cagcagggtgg gctccaagtg tctcgatgtg 1020
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 ggttatcgct gcatctgtgc cgagggtctac aagcagatgg aaggcatctg tgtgaaggag 1140
 cagatcccag agtcagcagg ctcttcctca gagatgacag aagacgagg tgggtgtctg 1200
 cagcagatgt tctttggcat catcatctgt gcactggcca cgctggctgc taaggcgac 1260
 ttggtgttca ccgcacatctt cattggggct gtggggcca tgactggcta ctgggtgtca 1320
 gagcgcagtg accgtgtgct ggagggtttc atcaaggca gataatcgcg gccaccac 1380
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 acagggtgg ggcacatcaca gctccctctt gccagctgca tgctgccagt tcctgttctg 1740
 tggcaccac atccccacac cccattgcca cttatttattt catctcagga aataaagaaa 1800
 ggtcttgaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met	Ala	Pro	Trp	Pro	Pro	Lys	Gly	Leu	Val	Pro	Ala	Val	Leu	Trp	Gly
1														15	

Leu	Ser	Leu	Phe	Leu	Asn	Leu	Pro	Gly	Pro	Ile	Trp	Leu	Gln	Pro	Ser
20														30	

Pro	Pro	Pro	Gln	Ser	Ser	Pro	Pro	Pro	Gln	Pro	His	Pro	Cys	His	Thr
35													45		

Cys	Arg	Gly	Leu	Val	Asp	Ser	Phe	Asn	Lys	Gly	Leu	Glu	Arg	Thr	Ile
													55	60	

Arg Asp Asn Phe Gly Gly	Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu		
65	70	75	80
Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly			
85	90	95	
Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser			
100	105	110	
Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro			
115	120	125	
Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro			
130	135	140	
Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu			
145	150	155	160
Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly			
165	170	175	
Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys			
180	185	190	
Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His			
195	200	205	
Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro			
210	215	220	
Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His			
225	230	235	240
Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys			
245	250	255	
Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg			
260	265	270	
Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg			
275	280	285	
Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu			
290	295	300	
Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln			
305	310	315	320
Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr			
325	330	335	
Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala			
340	345	350	

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
 385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
 405 410 415

Ile Lys Gly Arg
 420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga

50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc

22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 112

atctgcttgt agccctcgac ac

22

<210> 113

<211> 1616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (1461)
 <223> a, t, c or g

<400> 113

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tgagaccctc ctgcagccctt ctcaaggac agccccactc tgcctttgc tcctccaggg 60
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cgggggccgc ctgaccgggg agcagctctt gggcagccctg ctgcggcagc tgcatctcaa 180
agaggtgccc accctggaca gggccgacat ggaggagctg gtcatccccca cccacgttag 240
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<210> 114
 <211> 366
 <212> PRT
 <213> Homo sapiens

<400> 114

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1															

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
 20 25 30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190

Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
 290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
 305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
 325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
 340 345 350

 Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
 355 360 365

 <210> 115
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 115
 aggactgccat taacttgccct g 21

 <210> 116
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 116
 ataggagttt aaggcaggct gc 22

 <210> 117
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 117
 tgtgtggaca tagacgagtg ccgcgtaccgc tactgccagc accgc 45

 <210> 118
 <211> 1857
 <212> DNA
 <213> Homo sapiens

 <400> 118
 gtctgttccc aggagtcctt cggcggttgt ttttgtcagtq qccctgatcgc gatggggaca 60
 aaggcgcaag tcgagaggaa actgttgtgc ctcttcataat tggcgatctt gtttgtctcc 120
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtgcagaat tcctgagaat 180

aatcctgtga	agttgtccctg	tgcctactcg	ggcttttctt	ctccccgtgt	ggagtggaaag	240
tttgaccaag	gagacaccac	cagactcggt	tgctataata	acaagatcac	agttccatat	300
gaggaccggg	tgaccttctt	gccaactgggt	atcaccttca	agtccgtgac	acggaaagac	360
actgggacat	acacttgtat	ggtctctgag	gaaggcggca	acagctatgg	ggaggtcaag	420
gtcaagctca	tcgtgcttgt	gcctccatcc	aagcctacag	ttaacatccc	ctcctctgcc	480
accattggga	accgggcagt	gctgacatgc	tcagaacaag	atggttcccc	accttctgaa	540
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agcaactctt	cctatgtcct	gaatcccaca	acaggagagc	tggtctttga	tccctgtca	660
gcctctgata	ctggagaata	cagctgtgag	gcacggaatg	ggtatggac	acccatgact	720
tcaaatgtcg	tgcgcatgga	agctgtggag	cggaatgtgg	gggtcatcg	ggcagccgtc	780
cttgc当地	tgattctcct	ggaaatcttgc	gtttttggca	tctgggttgc	ctatagccga	840
ggccactttg	acagaacaaa	gaaaggact	tcgagtaaga	aggtgattta	cagccagcct	900
agtgc当地	gtgaaggaga	attcaaacag	acctcgtcat	tcctgggtgt	agcctggtcg	960
gctcacccgc	tatcatctgc	atttgccta	ctcaggtgt	accggactct	ggcccctgat	1020
gtctgttagtt	tcacaggatg	ccttatttgc	cttctacacc	ccacaggccc	ccctacttct	1080
tcggatgtgt	tttaataat	gtcagctatg	tgccccatcc	tccttcatgc	cctccctccc	1140
tttccctacca	ctgctgagtg	gcctgaaact	tgtttaaagt	gtttattccc	catttctttg	1200
aggatcagg	aaggaatcct	ggtatgcca	ttgacttccc	ttctaagtag	acagcaaaaa	1260
tggc当地	cgcaggaaatc	tgcactcaac	tgccccatcg	gctggcaggg	atcttgaat	1320
aggtatcttgc	agcttggttc	tgggctctt	ccttgtgtac	tgacgaccag	ggccagctgt	1380
tctagagcgg	gaatttagagg	ctagagcggc	tgaaatgggt	gttgggtgat	gacactgggg	1440
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ctctgc当地	tccctctgaa	tacaagctga	ctgacattga	ctgtgtctgt	ggaaaatggg	1560
agcttcttgtt	gtggagagca	tagtaaattt	tcagagaact	tgaagccaaa	aggatttaaa	1620
accgctgctc	taaagaaaaag	aaaactggag	gctggcggca	gtggctcagc	cctgtatcc	1680
cagaggctga	ggcaggcgg	tcacctgagg	tcgggagttc	ggatcagcc	tgaccaacat	1740
ggagaaaaccc	tactggaaat	acaaagttag	ccaggcatgg	tggtgc当地	ctgttagtccc	1800
agctgctcag	gagcctggca	acaagagcaa	aactccagct	aaaaaaaaaa	aaaaaaaaaa	1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
 35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
 50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160
 Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
 165 170 175
 Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
 180 185 190
 Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
 195 200 205
 Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
 210 215 220
 Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
 225 230 235 240
 Ala Ala Val Leu Val Thr Leu Ile Leu Gly Ile Leu Val Phe Gly
 245 250 255
 Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
 260 265 270
 Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
 275 280 285
 Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
 290 295
 <210> 120
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe
 <400> 120
 tcgcggagct gtgttctgtt tccc
 <210> 121
 <211> 50

<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 121		
tgatcgcat ggggacaaag gcgcaggctc gagagggaaac ttttgtgcct		50
<210> 122		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 122		
acacctgggtt caaagatgg		20
<210> 123		
<211> 24		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 123		
taggaagagt tgctgaaggc acgg		24
<210> 124		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 124		
ttgccttact caggtgctac		20
<210> 125		
<211> 20		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		

oligonucleotide probe

<400> 125
 actcagcagt ggttagaaag 20

<210> 126
 <211> 1210
 <212> DNA
 <213> Homo sapiens

<400> 126
 cagcgcgtgg ccggcgccgc tgtgggaca gcatgagcgg cggttggatg ggcgcagggttg 60
 gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgtcgcc ctcggactag 120
 gcctggaggc cgccgcgagc cgcgttcca cccccaccc tgcccaggcc gcaggcccc 180
 gctcaggctc gtgcccaccc accaagttcc agtgcgcac cagtggctta tgcgtgcccc 240
 tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300
 ggattgagcc atgtacccag aaagggcaat gcccaccgc ccctggcctc ccctgcccct 360
 gcaccggcgt cagtgactgc tctggggaa ctgacaagaaa actgcgcac tgcagccgccc 420
 tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
 ggcgctgcga cggccaccca gactgtcccg actccagcga cgagctcggc tggaaacca 540
 atgagatcct cccggaaggg gatgcaccaa ccatggggcc ccctgtgacc tggagagtg 600
 tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtccct 660
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 gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgcacc ccctccctt 780
 tgcctggct ccgagcccgag gagcgccctcc gcccactggg gttactggg gccatgaagg 840
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 ccgtcactca gccctggcg tagccggaca ggaggagagc agtgatgcgg atgggtaccc 960
 gggcacacca gccctcagag acctgagttc ttctggccac gtggaaacctc gaaccggagc 1020
 tcctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080
 agctaggatg gggAACCTGC cacagccaga actgagggggc tggccccagg cagctccaa 1140
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 aagttgttc 1210

<210> 127
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 127
 Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
 1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
 20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
 35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
 50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
 65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
 85 90 95

 Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
 100 105 110

 Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
 115 120 125

 Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
 130 135 140

 Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
 145 150 155 160

 Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
 165 170 175

 Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
 180 185 190

 Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
 195 200 205

 Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
 210 215 220

 Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala
 225 230 235 240

 Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln
 245 250 255

 Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
 260 265 270

 Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
 275 280

 <210> 128
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

 <400> 128
 aagttccagt gccgcaccag tggc

 <210> 129

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 129
ttggttccac agccgagctc gtcg                                24

<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 130
gaggaggagt gcaggattga gccatgtacc cagaaaggc aatgccacc      50

<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1837)
<223> a, t, c or g

<400> 131
cccacgcgtc cggtctcgct cgctcgcgca gcggggcgag cagaggtcgc gcacagatgc 60
ggtagact ggcggggggg ggaggcggag qagggaaagga agctgcgtgc atgagaccca 120
cagactcttg caagctggat gcccctgtg gatgaaaagat gtatcatgaa atgaacccga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcttg tggtttcggc tggcgctgtc ttccggccct gcacagctca 300
cggggggtt cgatgacctt caagtgtgtc ctgacccgg cattcccgag aatggttca 360
ggaccccccag cggagggggtt ttctttaaag gctctgttagc ccgatttcac tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tgggtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtataat tccatctgtc tgcaagaaga ttggcgatcc cctcaaattcg 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaatc atcacttgtc 600
atgaaggatt caagatccgg taccccgacc tacacaatat gttttcatta tgtcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctccctccc ggtggggact gtgatctcct 780
atcgctgttt tcccgattt aaacttgatg ggtctcgta ttttgatgtc ttacaaaacc 840
ttatctggtc gtccagccca ccccggtgcc ttgctctgga agcccaagtc tgtccactac 900
ctccaatggt gagtcacgga gatttcgtct gccacccgcg gccttgtgag cgctacaacc 960
acggaactgt ggtggagtt tactgcgtc ctggctacag cctcaccaggc gactacaagt 1020
acatcacctg ccagtatgga gatgtggttc cttcttatca agtctactgc atcaaattcg 1080
agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaaaggatt gtggcgatc 1140

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cgccaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
 agtcaaggc ccacttccc cccagggggc ctccccggag ttcacgact gaccctgact 1260
 ttgtggtgtt agacggcggtg cccgtcatgc tcccgtccta tgacgaagt gtgagtggcg 1320
 gcttgagtgc ctttaggcccc gggtacatgg cctctgtggg ccagggctgc cccttacccg 1380
 tggacgacca gagcccccca gcatacccg gtcagggga cacggacaca ggcccagggg 1440
 agtcagaaac ctgtgacagc gtctcaggct cttctgagct gtcacaaagt ctgtattcac 1500
 ctcccagggtg ccaagagagc acccaccctg ctccggacaa ccctgacata attgccagca 1560
 cggcagagga ggtggcatcc accagccag gcatccatca tgcccactgg gtgtgttcc 1620
 taagaaactg attgataaa aaatttccca aagtgcctg aagtgtctc tcaaatacat 1680
 gttgatctgt ggagttgatt ctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
 ctgatccta aaattgctat gctgatagag tggtagggc tggaaagctt atcaagtcct 1800
 gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132
 <211> 490
 <212> PRT
 <213> Homo sapiens

<400> 132
 Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
 1 5 10 15

Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
 50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
 85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
 130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
 145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

180	185	190
Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr		
195	200	205
Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys		
210	215	220
Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu		
225	230	235
Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe		
245	250	255
Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val		
260	265	270
Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr		
275	280	285
Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys		
290	295	300
Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr		
305	310	315
Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu		
325	330	335
Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His		
340	345	350
Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe		
355	360	365
Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala		
370	375	380
Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val		
385	390	395
Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr		
405	410	415
Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys		
420	425	430
Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro		
435	440	445
Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile		
450	455	460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
485 490

<210> 133
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 133
atctcctatac gctgctttcc cg 23

<210> 134
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 134
agccaggatc gcagtaaaac tcc 23

<210> 135
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 135
atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct 50

<210> 136
<211> 1815
<212> DNA
<213> Homo sapiens

<400> 136
cccacgcgtc cgctccgcgc cctccccccc gcctcccgta cggtccgtcg gtggcctaga 60
gatgctgtcg ccgcgggtgc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120
ccgttagcgcc cgagtgtcg cgggcgcacc cgagtccggc catgaggccg ggaaccgcgc 180
tacaggccgt gctgctggcc gtgctgtgg tggggctgca ggccgcgacg ggtcgccctgc 240
tqaqtqccctc qqatttqqac ctcaqaqqaq qqcaqccagt ctgcggggga gggacacaga 300

ggccttgtta taaagtcat tacttccatg atacttcgt aagactgaac tttgaggaag 360
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcg catcgagtct gaagatgaac 420
 agaaaactgat agaaaagtgc attgaaaacc tcttgcacat tgatgggtgac ttctggattg 480
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac cttagatgctt 540
 ggactgatgg cagcatatca caattnagga actggatgt ggatgagccg tcctgcggca 600
 gcgaggtctg cgtggcatg taccatcagc catcggcacc cgctggcatc ggaggccccct 660
 acatgttcca gtggaatgat gaccgggtca acatgaagaa caatttcatt tgcaaatatt 720
 ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
 cacctgtact tccagaagaa acacaggaag aagatgcca aaaaacattt aaagaaaagta 840
 gagaagctgc cttgaatctg gcttacatcc taatccccag cattccccctt ctccctcc 900
 ttgtggtcac cacagtgtt tttgggttt ggatctgttag aaaaagaaaa cgggagcagc 960
 cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag gaaacagcc 1020
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080
 ggcagacactt gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
 tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggtt gtgactctgg 1200
 tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctccca gaccaaatgg 1260
 ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320
 aaactgaaac tgacaacaat gaaaaagaaaa tgataagcaa aatccctcta ttttctataa 1380
 ggaaaataca cagaaggctt atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
 tccccacgac ctccctgttg acccccacgt tttggctgta tcctttatcc cagccagtca 1500
 tccagctcga cctttagata aggtacctt cccaggtctg gcacatagta gagtctcaat 1560
 aaatgtcact tgggtggtt tatctaactt ttaagggaca gagctttacc tggcagtgtat 1620
 aaagatgggc tggagctt gaaaaaccac ctcttttc ctgctctat acagcagcac 1680
 atattatcat acagacagaa aatccagaat ctttcaaag cccacatatg gtagcacagg 1740
 ttggcctgtg catcggaat tctcatatct gtttttca aagaataaaa tcaaataaaag 1800
 agcaggaaaa aaaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met	Arg	Pro	Gly	Thr	Ala	Leu	Gln	Ala	Val	Leu	Leu	Ala	Val	Leu	Leu
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Val	Gly	Leu	Arg	Ala	Ala	Thr	Gly	Arg	Leu	Leu	Ser	Ala	Ser	Asp	Leu
					20				25				30		

Asp	Leu	Arg	Gly	Gly	Gln	Pro	Val	Cys	Arg	Gly	Gly	Thr	Gln	Arg	Pro
					35			40				45			

Cys	Tyr	Lys	Val	Ile	Tyr	Phe	His	Asp	Thr	Ser	Arg	Arg	Leu	Asn	Phe
					50			55			60				

Glu	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Arg	Asp	Gly	Gly	Gln	Leu	Val	Ser
					65			70			75		80		

Ile	Glu	Ser	Glu	Asp	Glu	Gln	Lys	Leu	Ile	Glu	Lys	Phe	Ile	Glu	Asn
					85			90			95				

Leu	Leu	Pro	Ser	Asp	Gly	Asp	Phe	Trp	Ile	Gly	Leu	Arg	Arg	Arg	Glu
					100			105			110				

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
 115 120 125
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
 130 135 140
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
 145 150 155 160
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
 165 170 175
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
 180 185 190
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
 195 200 205
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
 210 215 220
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
 225 230 235 240
 Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
 245 250 255
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
 260 265 270
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
 275 280 285
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
 290 295 300
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly
 305 310 315 320
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
 325 330 335
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
 340 345 350
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
 355 360 365
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
 370 375 380

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<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 138
gttcattgaa aacctttgc catctgatgg tgacttctgg attggctca      50

<210> 139
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 139
aagccaaaga agcctgcagg aggg      24

<210> 140
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 140
cagtccaagc ataaagggtcc tggc      24

<210> 141
<211> 1514
<212> DNA
<213> Homo sapiens

<400> 141
ggggctcccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60
gcatccgcag gttcccgccg acttgggggc gcccgcgtg ccccgccgcg cgcagaagac 120
ttgtgtttgc ctccctgcgc ctcacccggg agggcagcga gggcctacca ccatgatcac 180
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cctgcaccag cggcggtgg ccctggccga gctgcaggag gccgatggcc agtgtccgg 300
cgaccgcagc ctgctgaagt taaaaatggt gcaggctgt tttcgacacg gggctcgag 360
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<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
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Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
 20 25 30

Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
 35 40 45

Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
 50 55 60

Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
 65 70 75 80

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
 85 90 95

Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
 100 105 110

Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
 115 120 125

Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
 130 135 140

Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
 145 150 155 160

Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
 165 170 175

Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
 180 185 190

 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys
 195 200 205

 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
 210 215 220

 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
 225 230 235 240

 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
 245 250 255

 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
 260 265 270

 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
 275 280 285

 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
 290 295 300

 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
 305 310 315 320

 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
 325 330 335

 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
 340 345 350

 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
 355 360 365

 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
 370 375 380

 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
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 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
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 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
 420 425

<210> 143
 <211> 24
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 143
      ccaactacca aagctgctgg agcc                                24

<210> 144
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 144
      gcagctctat taccacggga agga                                24

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 145
      tccttcccggt ggtaatagag ctgc                                24

<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe

<400> 146
      ggcagagaaac cagaggccgg aggagactgc ctctttacag ccagg      45

<210> 147
<211> 1686
<212> DNA
<213> Homo sapiens

<400> 147
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      ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtggg 180

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<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

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Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
 35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
 100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
 115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
 195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
 245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
 275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
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Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val
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<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

<400> 149		
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<211> 24		
<212> DNA		
<213> Artificial Sequence		
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<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 150		
ggctcataca aaataccact aggg		24
<210> 151		
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<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Synthetic		
oligonucleotide probe		
<400> 151		
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt		50
<210> 152		
<211> 1427		
<212> DNA		
<213> Homo sapiens		
<400> 152		
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<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

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Leu	Gly	Val	Phe	Gly	Leu	Phe	Arg	Leu	Leu	Gln	Trp	Val	Arg	Gly	Lys
															30
20								25							

Ala	Tyr	Leu	Arg	Asn	Ala	Val	Val	Val	Ile	Thr	Gly	Ala	Thr	Ser	Gly
35							40						45		

Leu	Gly	Lys	Glu	Cys	Ala	Lys	Val	Phe	Tyr	Ala	Ala	Gly	Ala	Lys	Leu
50						55						60			

Val	Leu	Cys	Gly	Arg	Asn	Gly	Gly	Ala	Leu	Glu	Glu	Leu	Ile	Arg	Glu
65						70				75			80		

Leu	Thr	Ala	Ser	His	Ala	Thr	Lys	Val	Gln	Thr	His	Lys	Pro	Tyr	Leu
85								90					95		

Val	Thr	Phe	Asp	Leu	Thr	Asp	Ser	Gly	Ala	Ile	Val	Ala	Ala	Ala	Ala
100							105					110			

Glu	Ile	Leu	Gln	Cys	Phe	Gly	Tyr	Val	Asp	Ile	Leu	Val	Asn	Asn	Ala
115							120					125			

Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Ile	Met	Asp	Thr	Thr	Val	Asp	Val	Asp
130							135					140			

Lys	Arg	Val	Met	Glu	Thr	Asn	Tyr	Phe	Gly	Pro	Val	Ala	Leu	Thr	Lys
145						150				155			160		

Ala	Leu	Leu	Pro	Ser	Met	Ile	Lys	Arg	Arg	Gln	Gly	His	Ile	Val	Ala
165								170					175		

Ile	Ser	Ser	Ile	Gln	Gly	Lys	Met	Ser	Ile	Pro	Phe	Arg	Ser	Ala	Tyr
180							185					190			

Ala	Ala	Ser	Lys	His	Ala	Thr	Gln	Ala	Phe	Phe	Asp	Cys	Leu	Arg	Ala
195							200					205			

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

210	215	220
Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg 225	230	235
Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu 245	250	255
Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val 260	265	270
Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu 275	280	285
Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu 290	295	300
Arg Lys Ser Lys Asn Ser 305	310	

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 154
ggtgctaaac tggtgctctg tggc 24

<210> 155
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 155
cagggcaaga tgagcattcc 20

<210> 156
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

Met	Lys	Phe	Leu	Leu	Asp	Ile	Leu	Leu	Leu	Pro	Leu	Leu	Ile	Val
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														30	
		20						25							

Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
															45
								35	40						

Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
															60
		50						55							

Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
															80
		65					70			75					

Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
															95
							85			90					

Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
															110
		100								105					

Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
															125
			115						120						

Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
															140
		130					135								

Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
															160
		145					150				155				

Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
															175
							165			170					

Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
															190
								180		185					

Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
															205
		195					200								

Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
															220
		210					215								

Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
															240
		225					230			235					

Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
															255
			245				250			255					

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
 275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
 290 295 300

<210> 160
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 160
ggtgaaggca gaaattggag atg 23

<210> 161
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 161
atccccatgca tcagcctgtt tacc 24

<210> 162
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 162
gctgggttag tctatacacatc agatttgttt gctacacaag atcctcag 48

<210> 163
<211> 2076
<212> DNA
<213> Homo sapiens

<400> 163
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attgttcgc tggcctgat gatgcctggc ccctgtatcg ggctgtttcg ctccctatac 180
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 taacaaacaa agctgttaaca tcttttctg ccaataacag aagtttggca tgccgtgaag 1920
 gtgtttggaa atattattgg ataagaatag ctcaattatc ccaaataaaat ggatgaagct 1980
 ataatagttt tggggaaaag attctcaaattt gtataaagtc tttagaacaaa agaattctt 2040
 gaaataaaaaa tattatatat aaaaagtaaaa aaaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met	Val	Gly	Ala	Met	Trp	Lys	Val	Ile	Val	Ser	Leu	Val	Leu	Leu	Met
1															15

Pro	Gly	Pro	Cys	Asp	Gly	Leu	Phe	Arg	Ser	Leu	Tyr	Arg	Ser	Val	Ser
															30
20															

Met	Pro	Pro	Lys	Gly	Asp	Ser	Gly	Gln	Pro	Leu	Phe	Leu	Thr	Pro	Tyr
															45
35															

Ile	Glu	Ala	Gly	Lys	Ile	Gln	Lys	Gly	Arg	Glu	Leu	Ser	Leu	Val	Gly
															60
50															

Pro	Phe	Pro	Gly	Leu	Asn	Met	Lys	Ser	Tyr	Ala	Gly	Phe	Leu	Thr	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65	70	75	80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln			
85		90	95
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro			
100		105	110
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val			
115		120	125
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr			
130		135	140
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser			
145		150	155
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala			
165		170	175
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu			
180		185	190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys			
195		200	205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg			
210		215	220
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser			
225		230	235
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile			
245		250	255
Gly Leu Leu Asp Glu Lys Gln Lys Tyr Phe Gln Lys Gln Cys His			
260		265	270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu			
275		280	285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr			
290		295	300
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys			
305		310	315
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro			
325		330	335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly			
340		345	350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His
 435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
 450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 165

ttccatgcc a cctaaggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 166

tggatgagg t gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

aaggatgacc	ccaagttcca	ctcatacggt	tccctgcctt	tcggctgcac	ccggggccggg	1740
gtggaatacc	gccttcgtca	ggctgcgtac	ctggccaaagc	ctggggactc	actggcccag	1800
gccttcaata	tcaccagcca	ggacgatgtt	ctctttgcctt	tcttcctcaa	agggcagaag	1860
cagtatcacc	acccgccccg	tgactctgtcc	ctgtgtgcctt	tccctatccg	ggccatcaac	1920
ttgcagatca	aggagcgcct	gcagtcctgc	taccaggggcg	agggcaacct	ggagctcaac	1980
tggctgttgtt	ggaaggagacgt	ccagtgcacg	aaggcgccctg	tccccatcga	tgataacttc	2040
tgtggacttgg	acatcaacca	gcccctggga	ggctcaactc	cagtggaggg	cctgaccctg	2100
tacaccacca	gcagggaccg	catgacccct	gtggcctctt	acgtttacaa	cggttacaga	2160
gtgggttttg	tggggactaa	gagtggcaag	ctgaaaaagg	taagagtcta	tgagttcaga	2220
tgctccaatg	ccattcacct	cctcagcaaa	gagtccctct	tggaaaggtag	ctattggttg	2280
agatttaact	ataggcaact	ttatttctt	ggggaaacaaa	ggtaaatgg	ggaggtaaga	2340
aggggttaat	tttgtgactt	agcttctagc	tacttcctcc	agccatcagt	cattgggtat	2400
gtaaaggatg	caagcgtatt	tcaatatttc	ccaaacttta	agaaaaaaact	ttaagaaggt	2460
acatctqcaa	aaqcaaa					2477

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

<400> 170

Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
 1 5 10 15

Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
20 25 30

Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
35 40 45

Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
50 55 60

Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Val Trp Val
65 70 75 80

Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
85 90 95

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
100 105 110

Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
 115 120 125

Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
130 135 140

Asn	Lys	Ser	Arg	Tyr	Pro	Pro	Leu	Ile	Val	Gln	Pro	Cys	Ser	Glu	Val
145					150					155					160

Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
165 170 175

Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
 180 185 190
 Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
 195 200 205
 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
 210 215 220
 Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
 225 230 235 240
 Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
 245 250 255
 Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
 260 265 270
 Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
 275 280 285
 Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
 290 295 300
 Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
 305 310 315 320
 Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg
 325 330 335
 Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
 340 345 350
 Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
 355 360 365
 Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
 370 375 380
 Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
 385 390 395 400
 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
 405 410 415
 Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
 420 425 430
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
 435 440 445
 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450	455	460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr		
465	470	475
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly		
485	490	495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val		
500	505	510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys		
515	520	525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln		
530	535	540
Leu Tyr Phe Leu Gly Glu Gln Arg		
545	550	

<210> 171
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 171
 tggaataccg cctcctgcag

20

<210> 172
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 172
 cttctgccct ttggagaaga tggc

24

<210> 173
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 173
 ggactcactg gcccaggcct tcaatatcac cagccaggac gat 42

 <210> 174
 <211> 3106
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> modified_base
 <222> (1683)
 <223> a, t, c or g

 <400> 174
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 aacacgcgat gaccacgtgg agcctccggc ggaggccggc cccgacgctg ggactcctgc 120
 tgctggtcgt ctgggcctc ctggtgcctc gcaggctgga ctggagcacc ctggccctc 180
 tgcggctccg ccatcgacag ctggggctgc aggccaaggg ctgaaacttc atgctggagg 240
 attccacctt ctggatcttc gggggttcca tccactattt ccgtgtgccc agggagtact 300
 ggagggaccg cctgctgaag atgaaggcct gtggctgaa caccctcacc acctatgttc 360
 cgtggAACCT gcatgagcca gaaagaggca aatttgactt ctctggaaac ctggacctgg 420
 aggcccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggcccct 480
 acatctgcag tgagatggac ctggggggtc tgcccaactg gctactccaa gaccctggca 540
 tgaggctgag gacaacttac aagggtttca cccaaggcgt ggacctttat tttgaccacc 600
 ttagtgtccag ggtgggtccca ctccagttaca agcgtgggg acctatcatt gccgtgcagg 660
 tggagaatga atatggttcc tataataaaag accccgcata catgccctac gtcaagaagg 720
 cactggagga ccgtggcatt gtggaaactgc tcctgacttc agacaacaag gatggctga 780
 gcaaggggat tgtccaggga gtcttggcca ccatcaactt gcagtcaaca cacgagctgc 840
 agctactgac cacctttctc ttcaacgtcc aggggactca gcccaagatg gtatggagg 900
 actggacggg gtggtttgc tcgtggggag gccctcacaa tatcttggat tcttctgagg 960
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 atgtcaccag ctatgactat gatgtgtgc tgacagaagc cggcgattac acggccaagt 1140
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 ggnntccct cccagaaaca cccacattac ctgtttttt ctgggttagc ttgtccatca 1740
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 tcaatggcca gaaccttggc cgttactggc acattggacc ccagaagacg ctttacctcc 1860
 caggtccctg gttgagcagc ggaatcaacc aggtcatcg ttttggaggag acgatggcgg 1920
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 cggtggcacc ccctcctgct ggtgccagtgg gtagactgcc gcctccctt gacctgaagc 2040
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cagaaaaagt gctgaaacgt gcccttgac cggacgtcac agccctgcga gcatctgctg 2340
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 gaagtgtgtc caagtccgca ttgagcctt gttctggggc ccagcccaac acctggcttg 3060
 ggctcaactgt cctgagttgc agtaaagcta taaccttgaa tcacaa 3106

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (539)

<223> Any amino acid

<400> 175

Met	Thr	Thr	Trp	Ser	Leu	Arg	Arg	Arg	Pro	Ala	Arg	Thr	Leu	Gly	Leu
1															

5

10

15

Leu	Leu	Leu	Val	Val	Leu	Gly	Phe	Leu	Val	Leu	Arg	Arg	Leu	Asp	Trp

20

25

30

Ser	Thr	Leu	Val	Pro	Leu	Arg	Leu	Arg	His	Arg	Gln	Leu	Gly	Leu	Gln

35

40

45

Ala	Lys	Gly	Trp	Asn	Phe	Met	Leu	Glu	Asp	Ser	Thr	Phe	Trp	Ile	Phe

50

55

60

Gly	Gly	Ser	Ile	His	Tyr	Phe	Arg	Val	Pro	Arg	Glu	Tyr	Trp	Arg	Asp

65

70

75

80

Arg	Leu	Leu	Lys	Met	Lys	Ala	Cys	Gly	Leu	Asn	Thr	Leu	Thr	Thr	Tyr

85

90

95

Val	Pro	Trp	Asn	Leu	His	Glu	Pro	Glu	Arg	Gly	Lys	Phe	Asp	Phe	Ser

100

105

110

Gly	Asn	Leu	Asp	Leu	Glu	Ala	Phe	Val	Leu	Met	Ala	Ala	Glu	Ile	Gly

115

120

125

Leu	Trp	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ser	Glu	Met	Asp

130

135

140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
 325 330 335
 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
 340 345 350
 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
 355 360 365
 Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
 370 375 380
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
 385 390 395 400
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
 405 410 415
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
 435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
 465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
 485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
 500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
 515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
 530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
 545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
 565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
 580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
 595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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 aaggggagca aagccggct cggcccgagg cccccaggac ctccatctcc caatgttgg 180
 ggaatccgac acgtgacggt ctgtccgccc tctcagacta gaggagcgct gtaaaacgcca 240
 tggctcccaa gaagctgtcc tgcttcgtt ccctgctgct gccgctcagc ctgacgctac 300
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 tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcgg 420

tgcttgggc cgaccggct ttgaagatgc gatggagcgg cctcaacgc atacagttt 480
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gaccttacat ctgtcgagag tgggagatgg ggggtctccc atccctggtg cttcgaaaac 660
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<210> 177

<211> 654

<212> PRT

<213> *Homo sapiens*

<400> 177

Met. Ala P

1

SET BEG 1

卷二十一

Asp Arg G

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Val ser G
58

Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
 65 70 75 80

Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
 85 90 95

Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
 100 105 110

Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
 115 120 125

Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
 130 135 140

Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
 145 150 155 160

Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
 165 170 175

Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
 180 185 190

Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
 195 200 205

Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
 210 215 220

Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Val Asp Phe Gly Pro
 225 230 235 240

Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
 245 250 255

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr
 260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
 275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe
 290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly
 305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser
 325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile

340	345	350
Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro		
355	360	365
Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu		
370	375	380
Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu		
385	390	395
Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr		
405	410	415
Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val		
420	425	430
Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val		
435	440	445
Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr		
450	455	460
Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg		
465	470	475
Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro		
485	490	495
Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu		
500	505	510
Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys		
515	520	525
Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr		
530	535	540
Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly		
545	550	555
Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr		
565	570	575
Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu		
580	585	590
Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu		
595	600	605
Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu		
610	615	620

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 625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 178
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<210> 179
<211> 24
<212> DNA
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<220>
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<400> 179
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<210> 180
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
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<210> 181
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<223> Description of Artificial Sequence: Synthetic
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<400> 181
ccagctatga ctatgatgca cc 22

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<210> 182
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<220>
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<400> 182
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<210> 183
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<210> 184
<211> 1947
<212> DNA
<213> Homo sapiens

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 ttttcttact aaaaaaaaaaaaaaa 1947

<210> 185

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

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					20				25					30	

Ile	Pro	Leu	Lys	Glu	Tyr	Ser	Phe	Glu	Lys	Val	Arg	Glu	Glu	Ser	Ser
					35				40					45	

Phe	Ser	Asp	Ile	Pro	Asp	Val	Lys	Asn	Asp	Phe	Ala	Phe	Leu	Leu	His
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Met	Val	Asp	Gln	Tyr	Asp	Gln	Leu	Tyr	Ser	Lys	Arg	Phe	Gly	Val	Phe
					65			70			75			80	

Leu	Ser	Glu	Val	Ser	Glu	Asn	Lys	Leu	Arg	Glu	Ile	Ser	Leu	Asn	His
					85				90					95	

Glu	Trp	Thr	Phe	Glu	Lys	Leu	Arg	Gln	His	Ile	Ser	Arg	Asn	Ala	Gln
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Asp	Lys	Gln	Glu	Leu	His	Leu	Phe	Met	Leu	Ser	Gly	Val	Pro	Asp	Ala
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Val	Phe	Asp	Leu	Thr	Asp	Leu	Asp	Val	Leu	Lys	Leu	Glu	Leu	Ile	Pro
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Glu	Ala	Lys	Ile	Pro	Ala	Lys	Ile	Ser	Gln	Met	Thr	Asn	Leu	Gln	Glu
					145			150			155			160	

Leu	His	Leu	Cys	His	Cys	Pro	Ala	Lys	Val	Glu	Gln	Thr	Ala	Phe	Ser
					165				170				175		

Phe	Leu	Arg	Asp	His	Leu	Arg	Cys	Leu	His	Val	Lys	Phe	Thr	Asp	Val
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Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
 195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
 210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
 225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
 245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
 260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
 275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
 290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
 305 310 315 320

Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
 325 330 335

Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
 340 345 350

Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
 355 360 365

Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
 370 375 380

Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400

His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415

Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430

Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445

Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
 450 455 460

Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465	470	475	480
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<210> 190
<211> 607
<212> PRT
<213> *Homo sapiens*

<400> 190

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 35 40 45
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
 50 55 60
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
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 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
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 Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
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 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
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 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
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 245 250 255
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
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 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
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Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
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Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
 305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
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Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
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Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
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His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
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Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
 385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
 405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
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Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
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 450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
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Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
 485 490 495

Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
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Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
 515 520 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
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 ttataaaaaaa aagttttttt ttcttcatttataatggaaatggataatggaaatggatcccccattgtt 2280
 caaacgtttt aatttttaaa accttttgg ctctttgtatataacacttacatcccccattgtt 2340
 taaactcatt gtgcaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met	Arg	Pro	Gln	Glu	Leu	Pro	Arg	Leu	Ala	Phe	Pro	Leu	Leu	Leu
1														

Leu	Leu	Leu	Leu	Pro	Pro	Pro	Cys	Pro	Ala	His	Ser	Ala	Thr	
20														

Arg	Phe	Asp	Pro	Thr	Trp	Glu	Ser	Leu	Asp	Ala	Arg	Gln	Leu	Pro	Ala
35															

195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
 50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
 65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
 85 90 95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
 100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
 115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
 130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
 145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
 165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
 180 185 190

Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
 195 200 205

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
 210 215 220

Leu Trp Ser Asp Gly Asp Gly Ala Pro Asp Gln Tyr Trp Asn Ser
 225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
 245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
 260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
 275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
 290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
 305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
450 455 460

Asn Val Ile
465

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<210> 196
<211> 23
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 196
tggtttgacc aggccaagtt cgg

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<210> 197  
<211> 24  
<212> DNA  
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 197
qqattcatcc tcaaggaaga gcgg

<210> 198

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 198
aacttgcagc atcagccact ctgc 24

<210> 199
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 199
ttccgtgccc agcttcggta gcgagtggtt ctgggtggat tggca 45

<210> 200
<211> 2372
<212> DNA
<213> Homo sapiens

<400> 200
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gttccagaac tctccatccg gactagttat tgagcatctg cctctcatat caccagtgc 120
catctgaggt gttccctgg ctctgaaggg gttaggcacga tggccaggtg cttcagcctg 180
gtgttgcctc tcacttccat ctggaccacg aggctcctgg tccaaggctc tttgcgtgca 240
gaagagctt ccatccaggt gtcatgcaga attatggggta tcacccttgt gagcaaaaag 300
gcgaaccagc agctgaattt cacagaagct aaggaggcct gtaggctgct gggactaagt 360
ttggccggca aggaccaagt tcaaacagcc ttgaaaagcta gcttggaaac ttgcagctat 420
ggctgggttg gagatggatt cgtggtcata tcctaggatta gccccaaaccc caagtgtggg 480
aaaaatgggg tgggtgtcct gatttggaaag gttccagtga gcccacagtt tgcagcctat 540
tgttacaact catctgatac ttggactaac tctgtgcattc cagaaattat caccaccaaa 600
gatcccatat tcaacactca aactgcaaca caaaacaacag aatttattgt cagtgacagt 660
acctactcggtt ggcatcccc ttactctaca atacctgccctt ctactactac tcctcctgtct 720
ccagcttcca cttctattcc acggagaaaa aaattgattt gttcacaga agttttatg 780
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tcatcagttt ccagtggtaa aaaggccctcc tggctgtctg aggcttaggtg gggttgaagc 1500
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 gctctgaaag agaaaacacgt atcccacctg acatgtcctt ctgagccccgg taagagcaaa 1620
 agaatggcag aaaagtttag cccctgaaag ccatggagat ttcataact tgagacctaa 1680
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 cactgttag aacacacaca cttactttt ctggctctca ccactgctga tattttctct 1860
 aggaaatata cttttacaag taacaaaaat aaaaactctt ataaatttctt attttatct 1920
 gagttacaga aatgattact aagaagatt actcagtaat ttgtttaaaa agtaataaaa 1980
 ttcaacaaac atttgcgtaa tagtactat atgtcaagt ctgtgcaagg tattacactc 2040
 tgtaattgaa tattattcct caaaaaattt cacatagtag aacgctatct gggaaagctat 2100
 tttttcagt tttgatattt ctagcttac tacttccaaa ctaattttta ttttgctga 2160
 gactaatctt attcatttc tctaataatgg caaccattat aaccttaatt tattattaac 2220
 atacctaaga agtacattgt tacctctata taccaagca cattttaaaaa gtgccattaa 2280
 caaatgtatc actagccctc cttttccaa caagaaggaa ctgagagatg cagaatattt 2340
 tgtgacaaaaa aattaaagca tttagaaaaac tt 2372

<210> 201
 <211> 322
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Synthetic protein

<400> 201
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 Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
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 Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
 35 40 45
 Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
 50 55 60
 Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
 65 70 75 80
 Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
 85 90 95
 Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
 100 105 110
 Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
 115 120 125
 Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
 130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
 145 150 155 160
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
 165 170 175
 Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser
 180 185 190
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
 195 200 205
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
 210 215 220
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
 225 230 235 240
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
 245 250 255
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
 260 265 270
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
 275 280 285
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
 290 295 300
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
 305 310 315 320
 Glu Val

<210> 202
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 202
 gagctttcca tccaggtgtc atgc

24

<210> 203
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 203
gtcagtgaca gtacctactc gg 22

<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 204
tggaggcagga ggagtagtag tagg 24

<210> 205
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 205
aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt 50

<210> 206
<211> 1620
<212> DNA
<213> Homo sapiens

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<222> (973)
<223> a, t, c or g

<220>
<221> modified_base
<222> (977)
<223> a, t, c or g

<220>
<221> modified_base
<222> (996)
<223> a, t, c or g

<220>
<221> modified_base

<222> (1003)

<223> a_t_s or q

<400> 206

<210> 207

<211> 296

<212> PBT

<213> Homo sapiens

<400> 207

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Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Pro Leu Cys His Gly
35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
65 70 75 80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
 85 90 95
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 100 105 110
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
 115 120 125
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
 130 135 140
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
 145 150 155 160
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
 165 170 175
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
 180 185 190
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
 195 200 205
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
 210 215 220
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
 225 230 235 240
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
 245 250 255
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
 260 265 270
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
 275 280 285
 Asp Gly Glu Asn Lys Lys Asp Lys
 290 295
 <210> 208
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe
 <400> 208
 qcttqqatat tcqcatqqqc ctac

<210> 209
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 209
 tggagacaaat atccctgagg 20

<210> 210
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 210
 aacagttggc cacagcatgg cagg 24

<210> 211
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 211
 ccattgtatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212
 <211> 1985
 <212> DNA
 <213> Homo sapiens

<400> 212
 ggacagctcg cggccccca gagctctagc cgtcgaggag ctgcctgggg acgttgcgg 60
 tggggccccca gcctggcccg ggtcacccctg gcatgaggag atgggcctgt tgctcctgg 120
 cccattgtctc ctgtctggccg gctcttacgg actgcccttc tacaacggct tctactactc 180
 caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240
 gaagctggtg gtggagacac ccgaggagac cctgttccacc taccaagggg ccagtgtgtat 300
 cctgccctgc cgctaccgct acgagccggc cctggcttcc ccgcggcggtg tgcgtgtcaa 360
 atggtggaaag ctgtcgagaa acggggcccc agagaaggac gtgctgggttccatcggt 420
 gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480
 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540
 ggtcattgac gggctggagg atgaaagcgg tctgggtggag ctggagctgc ggggtgtgg 600

115	120	125
Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr 130	135	140
Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu 145	150	155
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg 165	170	175
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala 180	185	190
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly 195	200	205
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr 210	215	220
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro 225	230	235
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp 245	250	255
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu 260	265	270
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu 275	280	285
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys 290	295	300
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser 305	310	315
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu 325	330	335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr 340	345	350
Gly Val Tyr Cys Tyr Arg Gln His 355	360	
<210> 214		
<211> 18		
<212> DNA		
<213> Artificial Sequence		
<220>		

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 214

tgc~~t~~tcgct~~a~~ ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 215

ttcc~~c~~c~~t~~tgt~~g~~ gg~~t~~tg~~g~~ag

18

<210> 216

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 216

agg~~g~~ctggaa gccagttc

18

<210> 217

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 217

agcc~~c~~agt~~g~~ag gaaatgc~~g~~

18

<210> 218

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 218

tgtccaaagt acacacacacct gagg

24

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Ala			
Gln			
Gly	Lys	Pro	Ser
	20	25	
			30
Arg	Val	His	Gln
Ala			Ala
Ala		Pro	Leu
	35	40	
Ser			Asp
Ala		Pro	His
Ala			Asp
			Asp
His			Ala
Gly	Asn	Phe	Gln
		Tyr	Tyr
		Asp	His
		Glu	Glu
		Ala	Arg
		Phe	Gly
		Leu	Asp
		Thr	Gly
		Pro	Asp
		Glu	Gln
		Ser	Ala
		Gln	Arg
		Ala	Leu
Gly	Arg	Ile	Val
			Asp
			Arg
			Met
			Asp
			Arg
			Ala
			Gly
			Asp
			Gly
			Trp
Val	Ser	Leu	Ala
			Glu
			Leu
			Arg
			Ala
			Trp
			Ile
			Ala
			His
			Thr
			Gln
			Gln
			Arg
His	Ile	Arg	Asp
			Ser
			Val
			Ala
			Ala
			Trp
			Asp
			Thr
			Tyr
			Asp
			Thr
			Asp
Arg	Asp	Gly	Arg
			Val
			Gly
			Trp
			Glu
			Leu
			Arg
			Asn
			Ala
			Thr
			Tyr
			Gly
His	Tyr	Ala	Pro
			Gly
			Glu
			Phe
			His
			Asp
			Val
			Glu
			Asp
			Ala
			Glu
			Thr
Gln	Asp	Gly	Asp
			Ser
			Met
			Ala
			Thr
			Arg
			Glu
			Leu
			Thr
			Ala
			Phe
			Leu
His	Pro	Glu	Glu
			Phe
			Pro
			His
			Met
			Arg
			Asp
			Ile
			Val
			Ile
			Ala
			Glu
			Thr
Leu	Glu	Asp	Leu
			Asp
			Arg
			Asn
			Lys
			Asp
			Gly
			Tyr
			Val
			Gln
			Val
			Glu
Tyr	Ile	Ala	Asp
			Leu
			Tyr
			Ser
			Ala
			Glu
			Pro
			Gly
			Glu
			Glu
			Pro
			Ala
Trp	Val	Gln	Thr
			Glu
			Arg
			Gln
			Gln
			Phe
			Arg
			Asp
			Phe
			Arg
			Asp
			Leu
			Asn
Lys	Asp	Gly	His
			Leu
			Asp
			Gly
			Ser
			Glu
			Val
			Gly
			His
			Trp
			Val
			Leu
			Pro
Pro	Ala	Gln	Asp
			Gln
			Pro
			Leu
			Val
			Glu
			Ala
			Asn
			His
			Leu
			Leu
			His
			Glu

BIOCHEMICAL & BIOPHYSICAL RESEARCH COMMUNICATIONS

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 225
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 <210> 226
 <211> 2403
 <212> DNA
 <213> Homo sapiens

 <400> 226
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 ccagcctgtc tgctcgctt ttggcgcccc cgactccccg cggtgccggg ttgcacaccg 180
 atcctggct tcgctcgatt tgccgcgcag ggcctccca gacctagagg ggcgtggcc 240
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 cctctctccc aggtgtgagc agctatcag tcaccatgtc cgcagcctgg atccggctc 420
 tcggcctcggt tgggtgtctg ctgctgtgc cggggccgc ggcagcggag ggagccgctc 480
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 tctgcccagg gggctgcctt cttaggaaat tctctgtgtt tggaaacata gtatatgttt 600
 ctgtatcgag catatgtgg gctgtgtcc acaggggagt aatcagcaac tcagggggac 660
 ctgtacgagt ctatagcta cctggtcgag aaaactattc ctcagtagat gccaatggca 720
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 gtacacagga ggccacagga caagcagtgt ccacagcaca tcacccaaca ggttaaacgac 840
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 tgattgtgg aagcttaat attgggcagc gccgatttaa ttacagaag aatttttgtt 960
 gaaaagtggc tctaattttt ggaattttggaa cagaaggacc acatgtgggc cttgttcaag 1020
 ccagtgaaca tcccaaata gaattttact tgaaaaactt tacatcagcc aaagatgttt 1080
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<210> 227

<211> 550

<212> PRT

<213> Homo sapiens

<400> 227

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			20				25					30			

Thr	Cys	Phe	Thr	Arg	Gly	Leu	Asp	Ile	Arg	Lys	Glu	Lys	Ala	Asp	Val
	35				40				45						

Leu	Cys	Pro	Gly	Gly	Cys	Pro	Leu	Glu	Glu	Phe	Ser	Val	Tyr	Gly	Asn
	50				55				60						

Ile	Val	Tyr	Ala	Ser	Val	Ser	Ser	Ile	Cys	Gly	Ala	Ala	Val	His	Arg
	65				70				75				80		

Gly	Val	Ile	Ser	Asn	Ser	Gly	Gly	Pro	Val	Arg	Val	Tyr	Ser	Leu	Pro
	85				90					95					

Gly	Arg	Glu	Asn	Tyr	Ser	Ser	Val	Asp	Ala	Asn	Gly	Ile	Gln	Ser	Gln
	100				105					110					

Met	Leu	Ser	Arg	Trp	Ser	Ala	Ser	Phe	Thr	Val	Thr	Lys	Gly	Lys	Ser
	115				120					125					

Ser	Thr	Gln	Glu	Ala	Thr	Gly	Gln	Ala	Val	Ser	Thr	Ala	His	Pro	Pro
	130				135					140					

Thr	Gly	Lys	Arg	Leu	Lys	Lys	Thr	Pro	Glu	Lys	Lys	Thr	Gly	Asn	Lys
	145				150					155			160		

Asp	Cys	Lys	Ala	Asp	Ile	Ala	Phe	Leu	Ile	Asp	Gly	Ser	Phe	Asn	Ile
	165				170					175					

Gly	Gln	Arg	Arg	Phe	Asn	Leu	Gln	Lys	Asn	Phe	Val	Gly	Lys	Val	Ala
	180				185					190					

Leu	Met	Leu	Gly	Ile	Gly	Thr	Glu	Gly	Pro	His	Val	Gly	Leu	Val	Gln
	195				200					205					

Ala	Ser	Glu	His	Pro	Lys	Ile	Glu	Phe	Tyr	Leu	Lys	Asn	Phe	Thr	Ser
	210				215					220					

Ala	Lys	Asp	Val	Leu	Phe	Ala	Ile	Lys	Glu	Val	Gly	Phe	Arg	Gly	Gly
	225				230					235			240		

Asn	Ser	Asn	Thr	Gly	Lys	Ala	Leu	Lys	His	Thr	Ala	Gln	Lys	Phe	Phe
	245				250					255					

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
 260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
 275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
 290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
 305 310 315 320

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
 325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
 340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
 355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
 370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
 385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
 405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
 420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
 435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
 450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
 465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala His Asp Ala Gly Ile Thr Ile
 485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
 500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
 515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
 530 535 540

Phe Leu Glu Ser Gln Gln
 545 550

<210> 228
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 228
tggtctcgca caccgatc 18

<210> 229
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 229
ctgcgtgtcca caggggag 18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 230
ccttgaagca tactgctc 18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 231
gagatagcaa tttccgccc 18

<210> 232

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 232
 ttcctcaaga gggcagcc 18

<210> 233
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 233
 cttggcacca atgtccgaga ttcc 24

<210> 234
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 234
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235
 <211> 2586
 <212> DNA
 <213> Homo sapiens

<400> 235
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<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

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20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
 65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
 85 90 95

 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
 100 105 110

 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
 115 120 125

 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
 130 135 140

 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
 145 150 155 160

 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
 165 170 175

 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
 180 185 190

 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
 195 200 205

 Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
 210 215 220

 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
 225 230 235 240

 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
 245 250 255

 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
 260 265 270

 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
 275 280 285

 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
 290 295 300

 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
 305 310 315 320

 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
 325 330 335

 Pro Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
 340 345 350

<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 237
ggagctgcac cccttgc 17

<210> 238
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 238
ggaggactgt gccaccatga gagactcttc aaacccaagg caaaattgg 49

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 239
gcagagcgga gatgcagcgg cttg 24

<210> 240
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 240
ttggcagctt catggagg 18

<210> 241
<211> 18
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 241
cctggggaaa aatgcaac 18

<210> 242
 <211> 24
 <212> DNA
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 <223> Synthetic Oligonucleotide Probe

 <400> 242
 ctccagctcc tggcgcacct cctc 24

 <210> 243
 <211> 45
 <212> DNA
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 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 243
 ggctctcagc taccgcgcag gagcgaggcc accctcaatg agatg 45

 <210> 244
 <211> 3679
 <212> DNA
 <213> Homo Sapien

 <400> 244
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aataaaaaata aataataaca ataaaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser
 35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu
 50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu
65 70 75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly
80 85 90

Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe
95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu
110 115 120

Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His
140 145 150

Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser
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 Asn Leu Leu Arg Leu His Leu Asn Ser Asn Leu Leu Arg Ala Ile
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 Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met
 185 190 195
 Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg
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 Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu
 215 220 225
 Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu
 230 235 240
 Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg
 245 250 255
 Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys
 260 265 270
 Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu
 275 280 285
 His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser
 290 295 300
 Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu
 305 310 315
 Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala
 320 325 330
 Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn
 335 340 345
 Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn
 350 355 360
 Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys
 365 370 375
 Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile
 380 385 390
 Glu Pro Gln Ser Thr Leu Cys Ala Glu Pro Pro Asp Leu Gln Arg
 395 400 405
 Leu Pro Val Arg Glu Val Pro Phe Arg Glu Met Thr Asp His Cys

410	415	420
Leu Pro Leu Ile Ser Pro Arg Ser Phe Pro Pro Ser Leu Gln Val		
425	430	435
Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu		
440	445	450
Pro Glu Pro Glu Ile Tyr Trp Val Thr Pro Ala Gly Leu Arg Leu		
455	460	465
Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly		
470	475	480
Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr		
485	490	495
Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val		
500	505	510
Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu		
515	520	525
Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His		
530	535	540
Ile Leu Leu Ser Trp Val Thr Pro Pro Asn Thr Val Ser Thr Asn		
545	550	555
Leu Thr Trp Ser Ser Ala Ser Ser Leu Arg Gly Gln Gly Ala Thr		
560	565	570
Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr		
575	580	585
Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala		
590	595	600
Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr		
605	610	615
Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly		
620	625	630
Leu Ile Ala Ile Leu Ala Leu Ala Val Leu Leu Leu Ala Ala Gly		
635	640	645
Leu Ala Ala His Leu Gly Thr Gly Gln Pro Arg Lys Gly Val Gly		
650	655	660
Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser		
665	670	675

Ala Pro Ser Val Arg Val Val Ser Ala Pro Leu Val Leu Pro Trp
680 685 690

Asn Pro Gly Arg Lys Leu Pro Arg Ser Ser Glu Gly Glu Thr Leu
695 700 705

Leu Pro Pro Leu Ser Gln Asn Ser
710

<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgccatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaaccttgtcg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

gcaaggccaag gcgctgtttg agaagggtgaa gaagttccgg acccatgtgg 50

aggaggggga cattgtgtac cgccctctaca tgcggcagac catcatcaag 100

gtgatcaagt tcatcctcat catctgctac accgtctact acgtgcacaa 150

catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200
 accgcaccta ccgctgtgcc cacccccctgg ccacacttcc caagatcctg 250
 gcgtccttct acatcagcct agtcatcttc tacggcctca tctgcatgt 300
 cacactgtgg tggatgtac ggcgctccct caagaagtac tcgtttgagt 350
 cgatccgtga ggagagcagc tacagcgaca tccccgacgt caagaacgac 400
 ttgccttca tgctgcacct cattgaccaa tacgacccgc tctactccaa 450
 gcgcttcgccc gtcttcctgt cggaggtgag tgagaacaag ctgcggcagc 500
 tgaacctcaa caacgagtgg acgctggaca agctccggca gcggctcacc 550
 aagaacgcgc aggacaagct ggagctgcac ctgttcatgc tcagtggcat 600
 ccctgacact gtgtttgacc tggtgagct ggaggctc aagctggagc 650
 tgateccccga cgtgaccatc ccgccccagca ttgcccagct cacgggcctc 700
 aaggagctgt ggctctacca cacagcgcc aagattgaag cgctgcgt 750
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 cgggctgcgg gagctcaaacc gcctcaaggt gctgcggctc aagagcaacc 950
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 aaggacaaca acctcaagac catcgaggag atcatcagct tccagcacct 1200
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 gagtctcttg tcttaatgtat tatgtccatc cgtctgtccg tccatttgg 3250
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 agactcggtc acagtatcaa ataaaaatcta taacagaaaa aaaaaaaaaa 3400
 a 3401

<210> 250

<211> 546
 <212> PRT
 <213> Homo Sapien

<400> 250
 Met Arg Gln Thr Ile Ile Lys Val Ile Lys Phe Ile Leu Ile Ile
 1 5 10 15
 Cys Tyr Thr Val Tyr Tyr Val His Asn Ile Lys Phe Asp Val Asp
 20 25 30
 Cys Thr Val Asp Ile Glu Ser Leu Thr Gly Tyr Arg Thr Tyr Arg
 35 40 45
 Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe
 50 55 60
 Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr
 65 70 75
 Leu Trp Trp Met Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu
 80 85 90
 Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

95	100	105
Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro		
110	115	120
Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu		
125	130	135
Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp		
140	145	150
Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu		
155	160	165
Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp		
170	175	180
Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val		
185	190	195
Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu		
200	205	210
Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala		
215	220	225
Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp		
230	235	240
Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu		
245	250	255
Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr		
260	265	270
Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu		
275	280	285
Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp		
290	295	300
Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr		
305	310	315
Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr		
320	325	330
Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser		
335	340	345
Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn		
350	355	360

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His
 365 370 375

 Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile
 380 385 390

 Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu
 395 400 405

 Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys
 410 415 420

 Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe
 425 430 435

 Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala
 440 445 450

 Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln
 455 460 465

 Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln
 470 475 480

 Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile
 485 490 495

 Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly
 500 505 510

 Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp
 515 520 525

 Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg
 530 535 540

 Ala Asp Lys Glu Gln Ala
 545

 <210> 251
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 251
 caacaatgag ggcaccaagc 20

 <210> 252
 <211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 252
gatggctagg ttctggaggt tctg 24

<210> 253
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 253
caacctgcag gagattgacc tcaaggacaa caacctaag accatcg 47

<210> 254
<211> 1650
<212> DNA
<213> Homo Sapien

<400> 254
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gcgcctctccc gtccccgggt gttgtctgct gctgccgtg ctgtggggcc 100
tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150
tgggattatg tgacggtccg caaggatgcc tacatgttct ggtggctcta 200
ttatgccacc aactcctgca agaacttctc agaactgccctt ctggcatgt 250
ggcttcaggc cggtccaggc gttcttagca ctggatttgg aaacttttag 300
gaaattgggc cccttgacag tggatctaaa ccacggaaaa ccacctggct 350
ccaggctgcc agtctcctat ttgtggataa tcccgtgggc actgggttca 400
gttatgtgaa tggtagtggt gcctatgccca aggacctggc tatggtggt 450
tcagacatga tggttctcct gaagaccttc ttcagttgcc acaaagaatt 500
ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550
cagctggcat tggtagtggc ctttataagg ccattcagcg agggaccatc 600
aagtgcact ttgcgggggt tgccctgggt gattcctgga tctccctgt 650
tgattcggtg ctctcctggg gaccttacct gtacagcatg tctcttctcg 700

aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750
 gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800
 agaaaatgatc attgaacaga acacagatgg ggtgaacttc tataacatct 850
 taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900
 cagagccacc tagtttgtct ttgtcagcgc cacgtgagac acctacaacg 950
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 aacatggagg aggacttcat gaagccagtc attgcatttgc tggacgagg 1100
 gctggaggca gggatcaacg tgacgggtgtaaatggacag ctggatctca 1150
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 tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350
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 gggctggaga tgagctggtt tggccttggg gcacagagct gagctgaggc 1450
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 taaaaaaaaattt atttgtttt atcaaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu

1 5 10 15

Leu Leu Pro Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp

20 25 30

Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val

35 40 45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn
 50 55 60
 Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln
 65 70 75
 Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu
 80 85 90
 Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp
 95 100 105
 Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr
 110 115 120
 Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu
 125 130 135
 Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
 140 145 150
 Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser
 155 160 165
 Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu
 170 175 180
 Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly
 185 190 195
 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
 200 205 210
 Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys
 215 220 225
 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
 230 235 240
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys
 245 250 255
 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr
 260 265 270
 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser
 275 280 285
 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His
 290 295 300
 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

305	310	315
Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp		
320	325	330
Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe		
335	340	345
Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly		
350	355	360
Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp		
365	370	375
Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu		
380	385	390
Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp		
395	400	405
Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn		
410	415	420
Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser		
425	430	435
Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln		
440	445	450
Gln Glu		
<210> 256		
<211> 1100		
<212> DNA		
<213> Homo Sapien		
<400> 256		
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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg
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Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser

20

25

30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly
35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
 50 55 60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
65 70 75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
80 85 90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
 95 100 105

 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
 110 115 120

 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
 125 130 135

 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
 140 145 150

 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
 155 160 165

 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
 170 175 180

 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
 185 190 195

 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
 200 205 210

 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
 215 220 225

 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 230 235 240

 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
 245 250 255

 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
 260 265 270

 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
 275 280 285

 Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
 290 295 300

 Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
 305 310

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

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cgagccccga ccagcggagg acgctgcccc caggctgggt gtccctggc 150
cgtgcggacc ctgaggaaga gctgagtctc acctttgccc tgagacagca 200
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agttccggccc tacctccct gcctccagcc cctatgtcac cacagtggga 1200
ggcacatcct tccaggaacc tttccatc acaaatgaaa ttgttgacta 1250
tatcagtgggt ggtgggttca gcaatgtttt cccacggcct tcataccagg 1300
aggaagctgt aacgaagttc ctgagctcta gcccccacct gccaccatcc 1350
agttacttca atgccagtgcc cggtgcctac ccagatgtgg ctgcactttc 1400

tcatggctac tgggtggtca gcaacagagt gcccattcca tgggtgtccg 1450
 gaacctcgcc ctctactcca gtgtttgggg ggatcctatac cttgatcaat 1500
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 agccctgctg aaccctcaac tattgactgc tgcagacagc ttatctccct 1850
 aaccctgaaa tgctgtgagc ttgacttgac tcccaaccct accatgctcc 1900
 atcataactca ggtctcccta ctcctgcctt agattcctca ataagatgct 1950
 gtaactagca tttttgaat gcctctccct ccgcattctca tctttctctt 2000
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 cttacttag cttccaggc ttaacttctc tgactactct tgtcttcctc 2250
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 ttagatttt tgctcttctc agtttactca ttgtccctg gaacaaatca 2350
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 aatgattgat acctcaaatg taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met	Gly	Leu	Gln
Ala	Cys	Leu	Leu
Leu	Gly	Leu	Phe
			Ala
			Leu
			Ile
			Leu

1

5

10

15

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

20	25	30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu		
35	40	45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg		
50	55	60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln		
65	70	75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg		
80	85	90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala		
95	100	105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu		
110	115	120
Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly		
125	130	135
Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val		
140	145	150
Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro		
155	160	165
His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser		
170	175	180
Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly		
185	190	195
Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn		
200	205	210
Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln		
215	220	225
Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu		
230	235	240
Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala		
245	250	255
Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly		
260	265	270
Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala		
275	280	285

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly
 290 295 300
 Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser
 305 310 315
 Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp
 320 325 330
 Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met
 335 340 345
 Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp
 350 355 360
 Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg
 365 370 375
 Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly
 380 385 390
 Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp
 395 400 405
 Tyr Ile Ser Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser
 410 415 420
 Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His
 425 430 435
 Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro
 440 445 450
 Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg
 455 460 465
 Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val
 470 475 480
 Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser
 485 490 495
 Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln
 500 505 510
 His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser
 515 520 525
 Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro
 530 535 540
 Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu
 545 550 555

Cys

<210> 260
<211> 1638
<212> DNA
<213> Homo Sapien

<400> 260
ggcgcgcgct ctctccggc gcccacacct gtctgagcgg cgcagcgagc 50
cgcgccccgg gggggctgct cggcgcgaa cagtgtcggt catggcagg 100
atcccagggc tcctcttcct tctcttcttt ctgctctgtg ctgttggca 150
agtgagccct tacagtgc ccctggaaacc cacttggcct gcataaccgcc 200
tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300
taaggaaact ccactgccc cttacgaaga ggccaagcaa tatctgtctt 350
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcattc 400
tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcagg 500
tcagcatttt tggaaaggac ttccctgctca actaccctt ctcaacatca 550
gtgaagttat ccacgggctg caccggcacc ctgggtggcag agaagcatgt 600
cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 650
cccagaagct tcgagtgccc ttccctaaagc ccaagttaa agatgggtggt 700
cgaggggcca acgactccac ttcaagccatg cccgagcaga tgaaatttca 750
gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800
atgccaatga catcgccatg gattatgatt atgcccctct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctccctgctaa 900
gcagctgcca gggggcagaa ttcaattctc tggttatgac aatgaccgac 950
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ttggcattt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150
gatttcaacg tggctgtcag aatcactcct ctcaaatatg cccagattg 1200
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ccaaattgtt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgtg 1350
tgtgtgttaag gtgtcttata atctttacc tatttcttac aattgcaaga 1400
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tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgttttg 1550
caaactttga ttttatttc atctgaactt gtttcaaaga tttatattaa 1600
atattqqca tacaqagat ataaaaaaaaaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu
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Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro
20 25 30

Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr
35 40 45

Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu
50 55 60

Val Ser Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu
65 70 75

Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu
 80 85 90

Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile

95 100 105

Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser
110 115 120

Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser
 125 130 135
 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe
 140 145 150
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val
 155 160 165
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
 170 175 180
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu
 185 190 195
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr
 200 205 210
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys
 215 220 225
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
 230 235 240
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro
 245 250 255
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys
 260 265 270
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
 275 280 285
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu
 290 295 300
 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala
 305 310 315
 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln
 320 325 330
 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp
 335 340 345
 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg
 350 355 360
 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly
 365 370 375
 Asn Tyr Leu Asp Cys Arg Glu Gly
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<210> 262
<211> 1378
<212> DNA
<213> Homo Sapien

<400> 262
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ccatgggtgg ttcgtggagcg ccccccagcccc tgggtgggggg ctgtctcgcc 100
accttcacactt ccctgctgtct gctggcgctcg acagccatcc tcaatgcggc 150
caggataacctt gttccccccag cctgtggaa gccccagcag ctgaaccggg 200
tttgtggcg cgaggacacgc actgacagcg agtggccctg gatcgtgagc 250
atccagaaga atgggaccca ccactgcgcga ggttctctgc tcaccagccg 300
ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
cggtccccaga aggtgggtgt tgccctgggtg gagccccacc ctgtgtattc 450
ctggaaggaa ggtgcctgtg cagacattgc cctggtgctgt ctcgagcgct 500
ccatacagtt ctcagagcgg gtcctgcccc tctgcctacc tgatgcctct 550
atccacacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600
ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650
ttcctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700
ggacagggac ccatcactga ggacatgctg tgtgcggct acttggaggg 750
ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800
tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850
gccgagcgca acaggccccgg ggtctacatc agcctctctg cgcaccgctc 900
ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950
gggggtggggc cctcaggggca ccgagccagg gctctggggc cgccgcgcgc 1000
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cacatctgga tctggatctg cggcgccctc gggcggtttc ccccgccgta 1100
aataggctca tctacacctta cctctggggg cccggacggc tgctgcggaa 1150

aggaaacccc ctcggccacc cgcccgacgg cctcaggccc ccctccaagg 1200
catcaggccc cgcccaacgg cctcatgtcc cggccccac gacttccggc 1250
cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300
ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350
ataaaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met	Val	Val	Ser	Gly	Ala	Pro	Pro	Ala	Leu	Gly	Gly	Gly	Cys	Leu
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Gly	Thr	Phe	Thr	Ser	Leu	Leu	Leu	Ala	Ser	Thr	Ala	Ile	Leu	
				20						25				30
Asn	Ala	Ala	Arg	Ile	Pro	Val	Pro	Pro	Ala	Cys	Gly	Lys	Pro	Gln
				35						40				45
Gln	Leu	Asn	Arg	Val	Val	Gly	Gly	Glu	Asp	Ser	Thr	Asp	Ser	Glu
				50					55					60
Trp	Pro	Trp	Ile	Val	Ser	Ile	Gln	Lys	Asn	Gly	Thr	His	His	Cys
				65						70				75
Ala	Gly	Ser	Leu	Leu	Thr	Ser	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
				80						85				90
Cys	Phe	Lys	Asp	Asn	Leu	Asn	Lys	Pro	Tyr	Leu	Phe	Ser	Val	Leu
				95					100					105
Leu	Gly	Ala	Trp	Gln	Leu	Gly	Asn	Pro	Gly	Ser	Arg	Ser	Gln	Lys
				110					115					120
Val	Gly	Val	Ala	Trp	Val	Glu	Pro	His	Pro	Val	Tyr	Ser	Trp	Lys
				125						130				135
Glu	Gly	Ala	Cys	Ala	Asp	Ile	Ala	Leu	Val	Arg	Leu	Glu	Arg	Ser
				140					145					150
Ile	Gln	Phe	Ser	Glu	Arg	Val	Leu	Pro	Ile	Cys	Leu	Pro	Asp	Ala
				155						160				165
Ser	Ile	His	Leu	Pro	Pro	Asn	Thr	His	Cys	Trp	Ile	Ser	Gly	Trp
				170					175					180

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
 185 190 195
 Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
 200 205 210
 Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
 215 220 225
 Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
 230 235 240
 Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
 245 250 255
 Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
 260 265 270
 Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
 275 280 285
 Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
 290 295 300
 Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala
 305 310 315
 Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 266
agctctagac caatgccagc ttcc 24

<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 267
gccaccaact cctgcaagaa ctttcagaa ctgcccctgg tcatg 45

<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 268
gggaaattca ccctatgaca ttgcc 25

<210> 269
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 271
gcggaagggc agaatggac tccaaag 26

<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagaga agggtgagac ccccg 24

<210> 275
<211> 45

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gcctctatcc tctctggcaa atgcagttac agcccgagc ccgac 45

<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
ggcaggat tccagggttc c 21

<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgcatt gctggtagag caag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 280
ttacagtgcc ccctggaaac ccacttggcc tgcataaccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281
cgtctcgagc gtcataaca gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctggcg actccggggg cccccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaagggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcg ggagcaggac agggacccat cactgaggac 100

atgctgttg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gtttctgctg 50

ccgctactgc tactgcttgt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgtttga tggtgagct gcacaacctc taccgggccc 150
 aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250
 caaggagcgc gggcgccgag gcgagaatct gttcgccatc acagacgagg 300
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 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550
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 cagaggctc aggctccctg gcaaccaagg ctctgcgtc tgtggaaacc 800
 caggccccaa cttccttagc aacgaaagac ccgcctcca tggcaacaga 850
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 gcctgcctc cttggatgag gagccagtta cttccccaa atcgaccat 950
 ttccctatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000
 ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050
 caagggact cttccccat gcccaggagg aggctgaggc tgaggctgag 1100
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 gccaggtag gtcaggcca cactggacca cacggggcac acctcctcca 1200
 agtccctgcc caattcccc aatacctctg ccaccgctaa tgccacgggt 1250
 gggcgtgccc tggctctgca gtcgtccttg ccaggtgcag agggccctga 1300
 caagccttagc gttgtgtcag ggctgaactc gggccctggc catgtgtggg 1350
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ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450
 catttcccc accctgtccc cagcccctaa acaagatact tcttggttaa 1500
 ggccctccgg aaggaaagg ctacggggca tgtgcctcat cacaccatcc 1550
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 ggactgcaca ccgggcccac acctctcctg cccctccctc ctgagtcctg 1650
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 gggattccta gggcagatg aaggacaagc cccactggag tggggttctt 1800
 tgagtggggg aggcaaggac gagggaaagga aagtaactcc tgactctcca 1850
 ataaaaacct gtccaaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu	
1									5					10	15

Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp
									20			25		30

Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala
									35			40		45

Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp
								50		55			60	

Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val
								65		70			75	

Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Gly	Glu	Asn	Leu	Phe	
								80		85			90	

Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu
						95				100			105	

Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys
								110		115			120	

Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala
								125		130			135	

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu
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Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr
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Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly
 170 175 180

Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser
 185 190 195

Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro
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Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser
 215 220 225

Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile
 230 235 240

Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys
 245 250 255

Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr
 260 265 270

Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr
 275 280 285

Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu
 290 295 300

Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
 305 310 315

Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
 320 325 330

Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly
 335 340 345

Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu
 350 355 360

Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
 365 370 375

Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr
 380 385 390

Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
 395 400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
 410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
 425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
 440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
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<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 286

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<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

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<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 288

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<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

<400> 289

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tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met Val Asp Val Leu Leu Leu Phe Ser Leu Cys Leu Leu Phe His
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Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
20 25 30

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
 35 40 45
 Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
 50 55 60
 Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
 65 70 75
 Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
 80 85 90
 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
 95 100 105
 Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
 110 115 120
 Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
 125 130 135
 Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
 140 145 150
 Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
 155 160 165
 Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
 170 175 180
 Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
 185 190 195
 Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
 200 205 210
 Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
 215 220 225
 Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
 230 235 240
 Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
 245 250 255
 Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
 260 265 270
 Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn
 275 280 285
 Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser

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Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg		
320	325	330
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala		
335	340	345
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn		
350	355	360
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys		
365	370	375
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys		
380	385	390
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln		
395	400	405
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly		
410	415	420
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp		
425	430	435
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala		
440	445	450
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser		
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Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu		
470	475	480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln		
485	490	495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu		
500	505	510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn		
515	520	525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn		
530	535	540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg		
545	550	555

Ala	Gly	Ala	Met	Ala	Arg	Leu	Glu	Cys	Ala	Ala	Val	Gly	His	Pro
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Ala	Pro	Gln	Ile	Ala	Trp	Gln	Lys	Asp	Gly	Gly	Thr	Asp	Phe	Pro
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Ala	Ala	Arg	Glu	Arg	Arg	Met	His	Val	Met	Pro	Glu	Asp	Asp	Val
590									595					600
Phe	Phe	Ile	Val	Asp	Val	Lys	Ile	Glu	Asp	Ile	Gly	Val	Tyr	Ser
605									610					615
Cys	Thr	Ala	Gln	Asn	Ser	Ala	Gly	Ser	Ile	Ser	Ala	Asn	Ala	Thr
620									625					630
Leu	Thr	Val	Leu	Glu	Thr	Pro	Ser	Phe	Leu	Arg	Pro	Leu	Leu	Asp
635									640					645
Arg	Thr	Val	Thr	Lys	Gly	Glu	Thr	Ala	Val	Leu	Gln	Cys	Ile	Ala
650									655					660
Gly	Gly	Ser	Pro	Pro	Pro	Lys	Leu	Asn	Trp	Thr	Lys	Asp	Asp	Ser
665									670					675
Pro	Leu	Val	Val	Thr	Glu	Arg	His	Phe	Phe	Ala	Ala	Gly	Asn	Gln
680									685					690
Leu	Leu	Ile	Ile	Val	Asp	Ser	Asp	Val	Ser	Asp	Ala	Gly	Lys	Tyr
695									700					705
Thr	Cys	Glu	Met	Ser	Asn	Thr	Leu	Gly	Thr	Glu	Arg	Gly	Asn	Val
710									715					720
Arg	Leu	Ser	Val	Ile	Pro	Thr	Pro	Thr	Cys	Asp	Ser	Pro	Gln	Met
725									730					735
Thr	Ala	Pro	Ser	Leu	Asp	Asp	Asp	Gly	Trp	Ala	Thr	Val	Gly	Val
740									745					750
Val	Ile	Ile	Ala	Val	Val	Cys	Cys	Val	Val	Gly	Thr	Ser	Leu	Val
755									760					765
Trp	Val	Val	Ile	Ile	Tyr	His	Thr	Arg	Arg	Arg	Asn	Glu	Asp	Cys
770									775					780
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro
785									790					795
Ser	Tyr	Leu	Ser	Ser	Gln	Gly	Thr	Leu	Ala	Asp	Arg	Gln	Asp	Gly
800									805					810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 815 820 825
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 830 835 840
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
 845 850 855
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 860 865 870
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 875 880 885
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 890 895 900
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 905 910 915
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 920 925 930
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 935 940 945
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
 950 955 960
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
 965 970 975
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
 980 985 990
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
 995 1000 1005
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
 1010 1015 1020
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
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 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
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 Asn Phe Gln Ser Tyr Asp Leu Asp Thr
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 <211> 2906

<212> DNA

<213> Homo Sapien

<400> 291

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<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Pro Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu
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35 40 45

Thr Cys Pro Ser Val Cys^oSer Cys Ser Asn Gln Phe Ser Lys Val
50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
65 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile
80 85 90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
95 100 . 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
110 115 120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
125 130 135

Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
140 145 150

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser

155	160	165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly		
170	175	180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly		
185	190	195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg		
200	205	210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp		
215	220	225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln		
230	235	240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile		
245	250	255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val		
260	265	270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp		
275	280	285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His		
290	295	300
Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp		
305	310	315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys		
320	325	330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp		
335	340	345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro		
350	355	360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys		
365	370	375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn		
380	385	390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val		
395	400	405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp		
410	415	420

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
 425 430 435
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro
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<211> 1119

<212> PRT

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<400> 294

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20														

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Ala	Ser	Ser	Met	Ser	His	Leu	Gln	Ser	Leu	Arg	Glu	Val	Lys	Leu
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95														

Asn	Asn	Asn	Glu	Leu	Glu	Thr	Ile	Pro	Asn	Leu	Gly	Pro	Val	Ser
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Ala	Asn	Ile	Thr	Leu	Leu	Ser	Leu	Ala	Gly	Asn	Arg	Ile	Val	Glu
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Asp	Leu	Ser	Ser	Asn	Asn	Ile	Ser	Glu	Leu	Gln	Thr	Ala	Phe	Pro
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Ser	Met	Glu	Pro	Gly	Tyr	Phe	Asp	Asn	Leu	Ala	Asn	Thr	Leu	Leu
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Val	Leu	Lys	Leu	Asn	Arg	Asn	Arg	Ile	Ser	Ala	Ile	Pro	Pro	Lys
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200														

Met	Phe	Lys	Leu	Pro	Gln	Leu	Gln	His	Leu	Glu	Leu	Asn	Arg	Asn
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Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly 275	280	285
Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn 290	295	300
Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu 305	310	315
Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser 320	325	330
Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn 335	340	345
Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser 350	355	360
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile 365	370	375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg 380	385	390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala 395	400	405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn 410	415	420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys 425	430	435
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Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln 455	460	465
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 ttctaaggaa aaaaatgata aaaatctcaa agctgatttt tcttggtata 3250
 gaaaaactaa tataaaagca ttatccctat ccctgcaaaa aaaaaa 3296

<210> 311
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 311
gcattggccg cgagactttg cc 22

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 312
gcggccacgg tccttgaaa tg 22

<210> 313
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 313
tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314
<211> 3003
<212> DNA
<213> Homo Sapien

<400> 314
gggagggggc tccggcgcc gcgcagcaga cctgctccgg ccgcgcgcct 50
cgccgctgtc ctccggagc ggcagcagta gccccggcgg cgagggctgg 100

gggttcctcg agactctcag aggggcgcct cccatcgcg cccaccaccc 150
caacctgttc ctgcgcgc actgcgctgc gccccaggac ccgctgccc 200
acatggattt tctcctggcg ctgggtctgg tatcctcgct ctacctgcag 250
gcggccgccc agttcgacgg gaggtggccc aggcaaatacg tgtcatcgat 300
tggcctatgt cggttatggtg ggaggattga ctgctgctgg ggctggcgc 350
gccagtcctg gggacagtgt cagcctgtgt gccaaccacg atgaaacat 400
ggtaatgtt tcgggccaaa caagtgcaga tgcatcctg gttatgctgg 450
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 tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900
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 tccaaatggc ctaataaaaa caattatgg taaataaaaa cactgttagt 3000
 aat 3003

<210> 315
 <211> 509
 <212> PRT
 <213> Homo Sapien

<400> 315
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Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val
 20 25 30

Ser Ser Ile Gly Leu Cys Arg Tyr Gly Gly Arg Ile Asp Cys Cys
 35 40 45

Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
 50 55 60

Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
 65 70 75

Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
 80 85 90

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
 95 100 105

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
 110 115 120

Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
 125 130 135

Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg
 140 145 150

Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
 155 160 165

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
 170 175 180
 Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
 185 190 195
 Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
 200 205 210
 Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
 215 220 225
 Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
 230 235 240
 Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr
 245 250 255
 Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
 260 265 270
 Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
 275 280 285
 Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro
 290 295 300
 Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr
 305 310 315
 Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro
 320 325 330
 Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr
 335 340 345
 Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala
 350 355 360
 Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln
 365 370 375
 Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val
 380 385 390
 His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu
 395 400 405
 Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly
 410 415 420
 Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys

425 430 435

Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly
440 445 450

Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser
455 460 465

Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala
470 475 480

Ala Leu Trp Gly Arg Asn Gly Gly His Trp Arg Gln Thr Gln
485 490 495

Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg
500 505

<210> 316
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 316
gatggttcct gctcaagtgc cctg 24

<210> 317
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 317
ttgcacttgt aggaccacg tacg 24

<210> 318
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 318
ctgatggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319
<211> 2110
<212> DNA

<213> Homo Sapien

<400> 319
cttcttgaa aaggattatc acctgatcag gttctctctg catttgcccc 50
tttagattgt gaaatgtggc tcaaggcttt cacaacttcc ctttccttgc 100
caacaggtgc ttgctcgaaa ctgaagggtga cagtgccatc acacactgtc 150
catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200
cactccagca tcagacatcc agatcatatg gctattttag agacccccaca 250
caatgccccaa atacttactg ggctctgtga ataagtctgt gtccctgac 300
ttgaaatacc aacacaagtt caccatgtatg ccacccaatg catctctgt 350
tatcaaccca ctgcagttcc ctgatgaagg caattacatc gtgaagggtca 400
acattcaggaaatgaaact ctatctgcca gtcagaagat acaagtcacg 450
gttcatgtatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500
ggctgtggag tatgtggggaa acatgaccct gacatgccat gtggaaagggg 550
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agtaaccaag gaagacattt ggaattacag ctgcctgggtg aggaaccctg 700
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tatggacttc aagtgaattt tgataaagggtt ctaaaagtagt gggaaagtgtt 800
tactgttgac cttggagagg ccatcctatt tgattttct gctgattctc 850
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aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050
cttgcacaga aaggaaaatc attgtcaccc tttagcaagta taactggaat 1100
atcaacccta caaagttata aaacagaaac tagaaggcag gccagaaaca 1150
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gaatacagga aagctcaaac attttcaggc catgaagatg ctctggatga 1250

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 aatcagtgaa gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550
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 tgaaaaactt acattgttcg attttcagc agactttgtt ttattaaatt 1850
 tttatttagt ttaagaatgc taaatttatg tttcaatttt atttccaaat 1900
 ttctatctt tatttgtac aacaaagtaa taaggatggt tgtcacaaaa 1950
 acaaaaactat gccttctctt tttttcaat caccagtagt atttttgaga 2000
 agacttgta acacttaagg aaatgactat taaagtctta tttttatttt 2050
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 aaaaaaaaaa 2110

<210> 320
 <211> 450
 <212> PRT
 <213> Homo Sapien

<400> 320				
Met Trp Leu Lys Val Phe Thr Thr Phe Leu Ser Phe Ala Thr Gly				
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20	25	30		
Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe				
35	40	45		
His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg				
50	55	60		

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
 65 70 75
 Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
 80 85 90
 Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
 95 100 105
 Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
 110 115 120
 Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
 125 130 135
 Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
 140 145 150
 Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
 155 160 165
 Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
 170 175 180
 Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
 185 190 195
 Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
 200 205 210
 Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
 215 220 225
 Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
 230 235 240
 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu
 245 250 255
 Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp
 260 265 270
 Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro
 275 280 285
 Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp
 290 295 300
 Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu
 305 310 315
 Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu

320	325	330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly		
335	340	345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp		
350	355	360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly		
365	370	375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His		
380	385	390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe		
395	400	405
Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro		
410	415	420
Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr		
425	430	435
Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu		
440	445	450

<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

gatcctgtca caaaaggccagt ggtgc 25

<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 323
ctccctctgg gctgtggagt atgtgggaa catgaccctg acatg 45

<210> 324
<211> 2397
<212> DNA
<213> Homo Sapien

<400> 324
gcaagcggcg aaatggcgcc ctccgggagt cttgcagttc ccctggcagt 50
cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100
acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150
tggatgatag aatttatgc cccgtggtgc cctgcttgc aaaaatcttca 200
accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250
ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatac 300
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ctatcagggt ccaaggacta agaaggactt cataaacttt ataagtgata 400
aagagtggaa gagtattgag cccgtttcat catggttgg tccaggttct 450
gttctgtatga gtagtatgtc agcactctt cagctatcta tgtggatcag 500
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gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850
cctagttaaa ttttatagtt atcttaatat tatgattttg ataaaaacag 900
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ttgcagggtt cagtctagat tgtcattaaa ttgaagagtc tacattcaga 1000

acataaaaagc actaggata caagttgaa atatgattt agcacagtat 1050
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tttggatgtg taacttgc tgccttagaa aaatatccta agcacaaaat 2350

aaacctttct aaccacttca ttaaagctga aaaaaaaaaa aaaaaaaa 2397
 <210> 325
 <211> 280
 <212> PRT
 <213> Homo Sapien
 <400> 325
 Met Ala Pro Ser Gly Ser Leu Ala Val Pro Leu Ala Val Leu Val
 1 5 10 15
 Leu Leu Leu Trp Gly Ala Pro Trp Thr His Gly Arg Arg Ser Asn
 20 25 30
 Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly
 35 40 45
 Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln
 50 55 60
 Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
 65 70 75
 Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly
 80 85 90
 Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
 95 100 105
 Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys
 110 115 120
 Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile
 125 130 135
 Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser
 140 145 150
 Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys
 155 160 165
 His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser
 170 175 180
 Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
 185 190 195
 Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
 200 205 210
 Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Leu Leu

215	220	225
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu		
230	235	240
Ala Asp Glu Glu Asp Val Ser Glu Glu Ala Glu Ser Lys Glu		
245	250	255
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser		
260	265	270
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser		
275	280	

<210> 326
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 326
tgaggtgggc aagcggcgaa atg 23

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 327
tatgtggatc aggacgtgcc 20

<210> 328
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 328
tgcagggttc agtcttagatt g 21

<210> 329
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 329

ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330

ggagtcttgc agttcccttg gcagtcctgg tgctgttgct ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331

gcgagtgtcc agctgcggag acccgtgata attcgtaac taattcaaca 50

aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taacccagtg 100

ggacaggcgg attggaagag cgggaaggtc ctggcccaga gcagtgtgac 150

acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200

ggtttggtgt cctgagctgt gtgcaggccg aattttcac ctctattggg 250

cacatgactg acctgattt a tgcagagaaa gagctggtgc agtctctgaa 300

agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350

ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgaggc 400

tacctggctc accctgtgaa tgcctacaaa ctggtaagc ggctaaacac 450

agactggct ggcgtggagg accttgcct gcaggactca gctgcagggt 500

ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550

gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600

ggacccaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650

caatgctgag tgtggatgac tgctttggga tggcccgctc ggcctacaat 700

gaaggggact attatcatac ggtgttggg atggagcagg tgctaaagca 750

gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800
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 ctcacccgcc gcctgctctc ctttgcacca agccacgaac gagctggagg 900
 gaatctgcgg tactttgagc agttatttggaa ggaagagaga gaaaaaacgt 950
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gttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150

cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

Met	Lys	Leu	Trp	Val	Ser	Ala	Leu	Leu	Met	Ala	Trp	Phe	Gly	Val
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Leu	Ser	Cys	Val	Gln	Ala	Glu	Phe	Phe	Thr	Ser	Ile	Gly	His	Met
			20						25					30

Thr	Asp	Leu	Ile	Tyr	Ala	Glu	Glu	Leu	Val	Gln	Ser	Leu	Lys
				35				40					45

Glu	Tyr	Ile	Leu	Val	Glu	Glu	Ala	Lys	Leu	Ser	Lys	Ile	Lys	Ser
				50				55					60	

Trp	Ala	Asn	Lys	Met	Glu	Ala	Leu	Thr	Ser	Lys	Ser	Ala	Ala	Asp
				65				70					75	

Ala	Glu	Gly	Tyr	Leu	Ala	His	Pro	Val	Asn	Ala	Tyr	Lys	Leu	Val
				80				85					90	

Lys	Arg	Leu	Asn	Thr	Asp	Trp	Pro	Ala	Leu	Glu	Asp	Leu	Val	Leu
				95				100					105	

Gln	Asp	Ser	Ala	Ala	Gly	Phe	Ile	Ala	Asn	Leu	Ser	Val	Gln	Arg
				110				115					120	

Gln	Phe	Phe	Pro	Thr	Asp	Glu	Asp	Glu	Ile	Gly	Ala	Ala	Lys	Ala
				125				130					135	

Leu	Met	Arg	Leu	Gln	Asp	Thr	Tyr	Arg	Leu	Asp	Pro	Gly	Thr	Ile
				140				145					150	

Ser	Arg	Gly	Glu	Leu	Pro	Gly	Thr	Lys	Tyr	Gln	Ala	Met	Leu	Ser
				155				160					165	

Val	Asp	Asp	Cys	Phe	Gly	Met	Gly	Arg	Ser	Ala	Tyr	Asn	Glu	Gly
				170				175					180	

Asp	Tyr	Tyr	His	Thr	Val	Leu	Trp	Met	Glu	Gln	Val	Leu	Lys	Gln
				185				190					195	

Leu	Asp	Ala	Gly	Glu	Glu	Ala	Thr	Thr	Lys	Ser	Gln	Val	Leu
				200				205					210

Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg
 215 220 225
 Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His
 230 235 240
 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu
 245 250 255
 Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu
 260 265 270
 Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro
 275 280 285
 Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys
 290 295 300
 Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His
 305 310 315
 Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu
 320 325 330
 Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met
 335 340 345
 Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys
 350 355 360
 Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr
 365 370 375
 Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp
 380 385 390
 Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile
 395 400 405
 Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn
 410 415 420
 Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg
 425 430 435
 Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala
 440 445 450
 Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr
 455 460 465
 Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr
 470 475 480

Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
485 490 495

Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
500 505 510

Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
515 520 525

Pro Cys Gly Ser Thr Glu Val Asp
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<210> 333
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 333
ccagggcacaa tttccaga 18

<210> 334
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 334
ggacccttct gtgtgccag 19

<210> 335
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 335
ggtctcaaga actcctgtc 19

<210> 336
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta cttg 24

<210> 337
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 337
gggcacatga ctgacacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338
<211> 2789

<212> DNA
<213> Homo Sapien

<400> 338
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agacaggaca atcttcttgg ggtatgttgtt cctggaaagcc agcgggcatt 200
gctctgtctt tggcctcatt gaccccaggat tctctggta aaactgaaag 250
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 ttttaata taaaaatgtt attaaacatg tcttctgcc 2789

<210> 339
<211> 772
<212> PRT
<213> Homo Sapien

<400> 339
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 20 25 30
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 35 40 45
 Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
 50 55 60
 Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
 65 70 75
 Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg
 80 85 90
 Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

95	100	105
Val Leu Thr Ser Arg Ala Thr Leu Ser	Thr Leu Ala Val Ala Val	
110	115	120
Asn Arg Thr Val Ala His His Phe Pro Arg	Leu Leu Tyr Phe Thr	
125	130	135
Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly	Met Gln Val Val Ser	
140	145	150
His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser	Glu Thr Leu Arg	
155	160	165
His Leu His Thr His Phe Gly Ala Asp	Tyr Asp Trp Phe Phe Ile	
170	175	180
Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg	Leu Ala Ala Leu	
185	190	195
Ala Gly His Leu Ser Ile Asn Gln Asp	Leu Tyr Leu Gly Arg Ala	
200	205	210
Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg	Tyr Cys His Gly	
215	220	225
Gly Phe Gly Tyr Leu Leu Ser Arg Ser	Leu Leu Leu Arg Leu Arg	
230	235	240
Pro His Leu Asp Gly Cys Arg Gly Asp	Ile Leu Ser Ala Arg Pro	
245	250	255
Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp	Ser Leu Gly Val Gly	
260	265	270
Cys Val Ser Gln His Gln Gly Gln Gln	Tyr Arg Ser Phe Glu Leu	
275	280	285
Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly	Ser Ser Ala Phe Leu	
290	295	300
Ser Ala Phe Ala Val His Pro Val Ser	Glu Gly Thr Leu Met Tyr	
305	310	315
Arg Leu His Lys Arg Phe Ser Ala Leu Glu	Leu Glu Arg Ala Tyr	
320	325	330
Ser Glu Ile Glu Gln Leu Gln Ala Gln	Ile Arg Asn Leu Thr Val	
335	340	345
Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser	Trp Pro Val Gly Leu	
350	355	360

Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp
 365 370 375

 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala
 380 385 390

 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp
 395 400 405

 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro
 410 415 420

 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg
 425 430 435

 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu
 440 445 450

 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg
 455 460 465

 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met
 470 475 480

 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu
 485 490 495

 Leu Val Ala Glu Ala Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe
 500 505 510

 Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu
 515 520 525

 Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp
 530 535 540

 Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg
 545 550 555

 Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala
 560 565 570

 Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro
 575 580 585

 Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly
 590 595 600

 Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp
 605 610 615

 Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu
 620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
 635 640 645
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
 650 655 660
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
 665 670 675
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
 680 685 690
 Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
 695 700 705
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
 710 715 720
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
 725 730 735
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
 740 745 750
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
 755 760 765
 Gln Glu Gln Ala Asn Ser Thr
 770

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

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cttttgaag ggtgtatgc ttggaagcat tttctgtgct ttgatcacta 150

tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200

catcatcacc tacaagctcc taacaaagaa gatatctga aaatttcaga 250

ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300

ttgtaaaacc caaagatgtg agtcttggg ctgcagtaaa ggagacttgg 350

accaaacact gtgacaaaagc agagttcttc agttctgaaa atgttaaagt 400

gttgagtca attaatatgg acacaaatga catgtggta atgatgagaa 450
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attaaagtga aagttgaaaa at 1572

<210> 341
<211> 318
<212> PRT
<213> Homo Sapien

<400> 341

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	20							25					30	
Gly	His	Gly	Asn	Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln
	35							40					45	
Ala	Pro	Asn	Lys	Glu	Asp	Ile	Leu	Lys	Ile	Ser	Glu	Asp	Glu	Arg
	50							55					60	
Met	Glu	Leu	Ser	Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val
	65							70					75	
Lys	Pro	Lys	Asp	Val	Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp
	80							85					90	
Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val
	95							100					105	
Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	Thr	Asn	Asp	Met	Trp	Leu
	110							115					120	
Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Phe	Asp	Lys	Tyr	Arg	Asp
	125							130					135	
Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	Thr	Phe	Ala	Ile
	140							145					150	
Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	Lys	Asp	Pro	Ser	Gln
	155							160					165	
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	170							175					180	
Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	Ser	Met	Lys
	185							190					195	
Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	Glu	Gln
	200							205					210	
Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	Val
	215							220					225	
Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala
	230							235					240	
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile
	245							250					255	
Lys	Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys

260 265 270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
275 280 285
Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly
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His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser
305 310 315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

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<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaatgc cctaaggcg 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345
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<210> 346
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<223> Synthetic Oligonucleotide Probe

<400> 346
gggatgcagg tggtgtctca tgggg 25

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 35 40 45

Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro
 50 55 60

Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser
 65 70 75

Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser
 80 85 90

Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu
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Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser
 110 115 120

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 125 130 135

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 140 145 150

Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp
 155 160 165

Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala
 170 175 180

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
185 190 195

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200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu
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gagtgcgaca tcgagagtt 20

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<213> Homo Sapien

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Met	Ala	Leu	Arg	Arg	Pro	Pro	Arg	Leu	Arg	Leu	Cys	Ala	Arg	Leu
1					5				10				15	

Pro	Asp	Phe	Phe	Leu	Leu	Leu	Phe	Arg	Gly	Cys	Leu	Ile	Gly
				20				25				30	

Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu
				35				40				45		

Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr
				50				55				60		

Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Ile	Gln	Asp	Glu	Gln	Thr
				65				70				75	

Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly
				80				85				90		

Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val
				95					100			105		

Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg
					110			115				120		

Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val
				125				130				135		

Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val
				140				145				150		

Pro	Val	Gly	Lys	Met	Ala	Thr	Leu	His	Cys	Gln	Glu	Ser	Gly
				155				160				165	

His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu
				170				175				180		

Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe
				185				190				195		

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
200 205 210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
230 235 240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
245 250 255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
275 280 285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly
290 295 300

Asp Phe Arg His Lys Ser Ser Phe Val Ile
305 310